Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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```
                                        GenCore version 5.1.6
                                        Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:              December 21, 2005, 12:44:31  ; Search time 54.0459 Seconds
                                                    (without alignments)
                                                    484.925 Million cell updates/sec

Title:               US-09-211-297-39
Perfect score:       1685
Sequence:            1 MRRASRDYTKYLRGSEEWGG..........LLDPDQDATYFGAFKVRDID 317
Scoring table:       BLOSUM62
                     Gapop 10.0 , Gapext 0.5

Searched:            572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:    572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing:     Minimum Match 0%
                     Maximum Match 100%
                     Listing first 45 summaries

Database :           Issued_Patents_AA:*
                     1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                     2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                     3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                     4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                     5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                     6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result                %       Query
No.     Score      Match  Length DB ID                    Description
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  1      1685      100.0   317  2   US-08-996-139-13       Sequence 13, Appl
  2      1685      100.0   317  2   US-08-995-659-13       Sequence 13, Appl
  3      1685      100.0   317  2   US-09-215-649A-13      Sequence 13, Appli
  4      1685      100.0   317  2   US-09-052-521C-4       Sequence 4, Appli
  5      1685      100.0   317  2   US-09-577-780-13       Sequence 13, Appli
  6      1685      100.0   317  2   US-09-577-800-13       Sequence 13, Appli
  7      1685      100.0   317  2   US-09-466-496-13       Sequence 13, Appl
  8      1685      100.0   317  2   US-09-871-856-13       Sequence 13, Appl
  9      1685      100.0   317  2   US-09-871-291-13       Sequence 13, Appl
 10      1685      100.0   317  2   US-09-396-937-2        Sequence 2, Appl
 11      1685      100.0   317  2   US-09-877-650-13       Sequence 13, Appl
 12      1685      100.0   317  2   US-09-865-363-13       Sequence 13, Appl
 13      1685      100.0   317  2   US-09-688-459-13       Sequence 13, Appl
 14      1685      100.0   317  2   US-09-957-944-6        Sequence 6, Appl
 15      1685      100.0   317  2   US-09-957-944-8        Sequence 8, Appl
 16      1424.5    84.5    316  1   US-08-842-842-7        Sequence 7, Appli
 17      1417.5    84.1    316  2   US-08-989-362-2        Sequence 2, Appli
 18      1417.5    84.1    316  2   US-09-052-521C-2       Sequence 2, Appli
 19      1417.5    84.1    316  2   US-09-671-658A-2       Sequence 2, Appli
 20      1417.5    84.1    316  2   US-09-396-937-4        Sequence 4, Appli
 21      1417.5    84.1    316  2   US-09-396-937-6        Sequence 6, Appli
 22      1326.5    78.7    294  2   US-08-996-139-11       Sequence 11, Appl
 23      1326.5    78.7    294  2   US-08-995-659-11       Sequence 11, Appl
 24      1326.5    78.7    294  2   US-09-215-649A-11      Sequence 11, Appl
 25      1326.5    78.7    294  2   US-09-577-780-11       Sequence 11, Appl
 26      1326.5    78.7    294  2   US-09-577-800-11       Sequence 11, Appl
 27      1326.5    78.7    294  2   US-09-466-496-11       Sequence 11, Appl
 28      1326.5    78.7    294  2   US-09-871-856-11       Sequence 11, Appl
 29      1326.5    78.7    294  2   US-09-871-291-11       Sequence 11, Appl
 30      1326.5    78.7    294  2   US-09-877-650-11       Sequence 11, Appl
 31      1326.5    78.7    294  2   US-09-865-363-11       Sequence 11, Appl
 32      1326.5    78.7    294  2   US-09-688-459-11       Sequence 11, Appl
 33       771      45.6    187  2   US-09-396-937-8        Sequence 8, Appli
 34       769      45.5    173  2   US-09-396-937-10       Sequence 10, Appl
 35       759      45.0    173  2   US-09-396-937-12       Sequence 12, Appl
 36       721.5    42.8    188  2   US-09-396-937-14       Sequence 14, Appl
 37       711.5    42.2    182  2   US-09-396-937-16       Sequence 16, Appl
 38       691      41.0    173  2   US-09-396-937-18       Sequence 18, Appl
 39       670      39.8    173  2   US-09-396-937-20       Sequence 20, Appl
 40       538      31.9    109  2   US-09-911-777-8        Sequence 8, Appli
 41       418      24.8    77   2   US-09-632-287A-11      Sequence 11, Appl
 42       418      24.8    77   2   US-10-286-696-11       Sequence 11, Appl
 43       363      21.5    77   2   US-09-632-287A-10      Sequence 10, Appl
 44       363      21.5    77   2   US-10-286-696-10       Sequence 10, Appl
 45       251.5    14.9    279  2   US-09-072-993C-3       Sequence 3, Appl
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                                    ALIGNMENTS

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RESULT 1
US-08-996-139-13
; Sequence 13, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Dirk M.
;  APPLICANT: Galibert, Laurent
;  APPLICANT: Maraskovsky, Eugene
;  TITLE OF INVENTION: Receptor Activator of NF-kappaB
;  NUMBER OF SEQUENCES: 19
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Immunex Corporation, Law Department
;  STREET: 51 University Street
;  CITY: Seattle
;  STATE: WA
;  COUNTRY: USA
;  ZIP: 98101
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: Apple Power Macintosh
;  OPERATING SYSTEM: Apple Operating System 7.5.5
;  SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/996,139
;  FILING DATE: 22 DECEMBER 1997
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: USSN 60/064,671
;  FILING DATE: 14 OCTOBER 1997
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: USSN 08/813,509
;  FILING DATE: 07 MARCH 1997
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: USSN 08/772,330
;  FILING DATE: 23 DECEMBER 1996
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Perkins, Patricia Anne
;  REGISTRATION NUMBER: 34,693
;  REFERENCE/DOCKET NUMBER: 2851-A
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (206)587-0430
;  TELEFAX: (206)233-0644
;  INFORMATION FOR SEQ ID NO: 13:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 317 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-08-996-139-13
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RESULT 2
US-08-995-659-13
Sequence 13, Application US/08995659
Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430

Query Match　　　　Score 1685; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 2e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    1 MRRASRDYTKYLRGSEEMGGGPGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy   61 VCSVALFPYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICPRHHETSGDLATEYLQLMV 240
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Db  181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICPRHHETSGDLATEYLQLMV 240

Qy  241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHYSINVGGFFKLRSGEEISIEVSNPSLLD 300
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Qy  301 PDQDATYFGAFKVRDID 317
        |||||||||||||||||
Db  301 PDQDATYFGAFKVRDID 317
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TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-659-13

Query Match　　　　Score 1685; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 2e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MRRASRDYTKYLRGSEEMGGGPGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRRASRDYTKYLRGSEEMGGGPGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy   61 VCSVALFPYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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Db   61 VCSVALFPYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy  121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
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Qy  181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICPRHHETSGDLATEYLQLMV 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy  301 PDQDATYFGAFKVRDID 317
        |||||||||||||||||
Db  301 PDQDATYFGAFKVRDID 317
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RESULT 3
US-09-215-649A-13
Sequence 13, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
　　Galibert, Laurent
　　Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 21, 2005, 12:35:06 ; Search time 218.262 Seconds
                   (without alignments)
                   1024.696 Million cell updates/sec

Title: US-09-211-297-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.........LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_05.80:*
               1: uniprot_sprot:*
               2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1685	100.0	317	1	TNF11_HUMAN	O14788; h tumor nec
2	1685	100.0	317	2	Q5T9Y4_HUMAN	Q5t9y4 homo sapien
3	1417.5	84.1	318	1	TNF11_MOUSE	O35235 m tumor nec
4	1396.5	82.9	316	1	TNF11_RAT	Q9ese2 r tumor nec
5	1292	76.7	244	2	Q54A98_HUMAN	Q54a98 homo sapien
6	559.5	33.2	290	2	Q5HZR8_XENLA	Q5hzr8 xenopus lae
7	470	27.9	117	2	Q5XLH0_RABIT	Q5xlh0 oryctolagus
8	273.5	16.2	289	2	Q4VSR6_PIG	Q4vsr6 sus scrofa
9	266	15.8	317	2	Q7ZYX9_BRARE	Q7zyx9 brachydanio
10	265	15.7	304	2	Q7T1F2_CHICK	Q7t1f2 gallus gall
11	262.5	15.6	292	2	Q5ZK93_CHICK	Q5zk93 gallus gall
12	251.5	14.9	281	1	TNF10_HUMAN	P50591 homo sapien
13	251.5	14.9	281	2	Q6IBA9_HUMAN	Q6iba9 homo sapien
14	249.5	14.8	299	2	Q6DHG9_BRARE	Q6dhg9 brachydanio
15	249.5	14.8	303	2	Q5XKN3_MOUSE	Q5xkn3 mus musculu
16	248	14.7	291	1	TNF10_MOUSE	P50592 mus musculu
17	245.5	14.6	264	2	Q4S9Q4_BRARE	Q4s9q4 tetraodon n
18	240.5	14.3	214	2	Q9DDZ5_BRARE	Q9ddz5 brachydanio
19	234	13.9	300	2	Q5U675_HUMAN	Q5u675 homo sapien
20	216.5	12.8	287	2	Q90WT9_CHICK	Q90wt9 gallus gall
21	215.5	12.8	287	2	Q8K3G0_RAT	Q8k3g0 rattus norv
22	211	12.5	285	2	Q4SKU4_TETNG	Q4sku4 tetraodon n
23	200	11.9	282	2	TNFL6_PIG	Q9bea8 sus scrofa
24	194.5	11.5	282	1	Q861W5_FELCA	Q861w5 felis silve
25	190.5	11.3	253	2	Q5CAQ0_CHICK	Q5caq0 gallus gall
26	189	11.2	281	2	TNFL6_HUMAN	P48023 h tumor nec
27	189	11.2	281	1	Q53ZZ1_HUMAN	Q53zz1 homo sapien
28	187.5	11.1	279	2	Q7TMV9_MOUSE	Q7tmv9 mus musculu
29	186	11.1	280	2	TNFL6_MACFA	P63309 m tumor nec
30	186	11.0	280	1	TNFL6_MACMU	P63307 m tumor nec
31	186	11.0	280	1	TNFL6_MACNE	P63306 m tumor nec
32	184.5	10.9	252	2	Q8K3Y8_MOUSE	Q8k3y8 mus musculu
33	184.5	10.9	279	1	TNFL6_MOUSE	P41047 mus musculu
34	184.5	10.9	279	2	Q54E9_MOUSE	Q54e9 mus musculu
35	182.5	10.8	278	2	Q4STX9_TETNG	Q4stx9 tetraodon n
36	182.5	10.8	280	1	TNFL6_CERTO	Q9bdn1 c tumor nec
37	181	10.7	95	2	Q6UWI7_HUMAN	Q6uwi7 homo sapien
38	181	10.7	95	2	Q6UY13_HUMAN	Q6uy13 homo sapien
39	179.5	10.7	252	2	Q80Y20_MOUSE	Q80y20 mus musculu
40	177.5	10.5	252	2	Q8K3Y7_RAT	Q8k3y7 rattus norv
41	176.5	10.5	261	1	TNFL5_BOVIN	P51749 b tumor nec
42	175.5	10.4	278	1	TNFL5_RAT	P36940 rattus norv
43	169.5	10.1	261	1	TNFL5_CALJA	Q9bdm3 c tumor nec
44	167.5	9.9	261	1	TNFL5_AOTTR	Q9bdn3 a tumor nec
45	162	9.6	239	2	Q5OL61_CHICK	Q5ol61 gallus gall

ALIGNMENTS

RESULT 1
TNF11_HUMAN

ID   TNF11_HUMAN   STANDARD;   PRT;   317 AA.
AC   O14788; O14723; Q96Q17; Q9P2Q3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF) [Contains: Tumor necrosis factor ligand
DE   superfamily member 11, membrane form; Tumor necrosis factor ligand
DE   superfamily member 11, soluble form].
GN   Name=TNFSF11; Synonyms=OPGL, RANKL, TRANCE;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Lymph node;
RX   MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow, and Peripheral blood;
RX   MEDLINE=98232661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RC   TISSUE=Tongue;
RX   MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;
RA   Ikeda T., Kuroyama H., Hirokawa K.;
RA   Nagai M., Kyakumoto S., Sato N.;
RT   "Determination of human RANKL isoforms.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC   TISSUE=Tongue;
RX   MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;
RT   "Cancer cells responsible for humoral hypercalcemia express mRNA
RT   encoding a secreted form of ODF/TRANCE that induces osteoclast
RT   formation.";

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RL   Biochem. Biophys. Res. Commun. 269:532-536(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 73-317.
     TISSUE=Thymocyte;
RX   MEDLINE=97460112; PubMed=9312123; DOI=10.1074/jbc.272.40.25190;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).
-!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
    TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
    Augments the ability of dendritic cells to stimulate naive T-cell
    proliferation. May be an important regulator of interactions
    between T cells and dendritic cells and may play a role in the
    regulation of the T cell-dependent immune response. May also play
    an important role in enhanced bone-resorption in humoral
    hypercalcemia of malignancy.
-!- SUBUNIT: Homotrimer. (By similarity).
-!- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
    Secreted (isoform 2). A soluble form of isoform 1 arises by
    proteolytic processing (By similarity).
-!- ALTERNATIVE PRODUCTS:
    Event=Alternative splicing; Named isoforms=3;
    Name=1;
      IsoId=O14788-1; Sequence=Displayed;
    Name=2; Synonyms=SODF;
      IsoId=O14788-2; Sequence=VSP_006447;
    Name=3;
      IsoId=O14788-3; Sequence=VSP_006446;
-!- TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
    spleen, peripheral blood leukocytes, bone marrow, heart, placenta,
    skeletal muscle, stomach and thyroid.
-!- INDUCTION: Up-regulated by T cell receptor stimulation.
-!- PTM: The soluble form of isoform 1 derives from the membrane form
    by proteolytic processing (By similarity). The cleavage may be
    catalyzed by ADAM17.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
-!- This Swiss-Prot entry is copyright. It is produced through a
    collaboration between the Swiss Institute of Bioinformatics and the
    European Bioinformatics Institute. There are no restrictions on its
    use as long as its content is in no way modified and this statement is not
    removed.
```

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DR   EMBL; AF019047; AAB86811.1; -; mRNA.
DR   EMBL; AF053712; AAC39731.1; -; mRNA.
DR   EMBL; AB064269; BAB79694.1; -; mRNA.
DR   EMBL; AB061227; BAB71768.1; -; mRNA.
DR   EMBL; AB064270; BAB79695.1; -; mRNA.
DR   EMBL; AB037599; BAA90488.1; -; mRNA.
DR   EMBL; BC074823; AAH74823.1; -; mRNA.
DR   EMBL; BC074890; AAH74890.1; -; mRNA.
DR   EMBL; AF013171; AAC51762.1; -; mRNA.
DR   HSSP; O35235; 1JTZ.
DR   SMR; O14788; 162-317.
DR   Ensembl; ENSG00000120659; Homo sapiens.
DR   HGNC; HGNC:11926; TNFSF11.
DR   MIM; 602642; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   GO; GO:0030316; P:osteoclast differentiation; NAS.
DR   InterPro; IPR006052; TNF family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD020012; TNF subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF; 1; FALSE_NEG.
DR   PROSITE; PS00049; TNF_2; 1.
DR   PROSITE; PS50049; TNF; 1.
KW   Alternative splicing; Cytokine; Developmental protein;
KW   Differentiation; Glycoprotein; Receptor; Signal-anchor; Transmembrane.
FT   CHAIN         1    317       Tumor necrosis factor ligand superfamily
FT                                member 11, membrane form.
FT   CHAIN       140    317       Tumor necrosis factor ligand superfamily
FT                                member 11, soluble form (By similarity).
FT   TOPO_DOM      1     47       Cytoplasmic (Potential).
FT   TRANSMEM     48     68       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     69    317       Extracellular (Potential).
FT   SITE        139    140       Cleavage (By similarity).
FT   CARBOHYD    171    171       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    198    198       N-linked (GlcNAc...) (Potential).
FT   VARSPLIC      1     73       Missing (in isoform 2).
FT                                /FTId=VSP_006447.
FT   VARSPLIC      1     47       Missing (in isoform 3).
FT                                /FTId=VSP_006446.
FT   CONFLICT    194    194       A -> G (in Ref. 6).
SQ   SEQUENCE   317 AA;  35478 MW;  76617644634809 7F CRC64;
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Query Match             100.0%;  Score 1685;  DB 1;  Length 317;
Best Local Similarity   100.0%;  Pred. No. 6.5e-136;
Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MRRASRDYTKYLRGSEEMGGPGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGPGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFPYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFPYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICRRHHETSGDLATEYLQLMV 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICRRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
          |||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

RESULT 2
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OM protein - protein search, using sw model

Run on: December 21, 2005, 12:34:10 ; Search time 215.664 Seconds
(without alignments)

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GenCore version 5.1.6.

645.834 Million cell updates/sec

Title: US-09-211-297-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG..........LLDPDQDATYFGAFKVRDID 317
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1685	100.0	317	2	AAW83195	Aaw83195 Human ost
2	1685	100.0	317	2	AAW69957	Aaw69957 NF-kB rec
3	1685	100.0	317	2	AAW68293	Aaw68293 NF-kB rec
4	1685	100.0	317	2	AAE08738	Aae08738 Human rec
5	1685	100.0	317	2	AAY84417	Aay84417 Amino aci
6	1685	100.0	317	4	AAE04426	Aae04426 Human rec
7	1685	100.0	317	4	AAE01993	Aae01993 Human ful
8	1685	100.0	317	4	ABB08134	Abb08134 Human RAN
9	1685	100.0	317	5	AAE26103	Aae26103 Human RAN
10	1685	100.0	317	5	ABG31631	Abg31631 Human RAN
11	1685	100.0	317	5	AAU78285	Aau78285 Human TRA
12	1685	100.0	317	5	AAO19096	Aao19096 C neoform
13	1685	100.0	317	5	ADR29336	Adr29336 Human RAN
14	1685	100.0	317	6	ABP55108	Abp55108 Human ost
15	1685	100.0	317	6	AAE34364	Aae34364 Human rec
16	1685	100.0	317	6	ABR42314	Abr42314 Human RAN
17	1685	100.0	317	6	ADB16988	Adb16988 Human rec
18	1685	100.0	317	7	ADC35204	Adc35204 Human TNF
19	1685	100.0	317	7	ADC73002	Adc73002 Human RAN
20	1685	100.0	317	7	ADC78268	Adc78268 Human RAN
21	1685	100.0	317	7	ABW02277	Abw02277 Human RAN
22	1685	100.0	317	7	ADG46723	Adg46723 Human RAN
23	1685	100.0	317	7	ADJ82112	Adj82112 Protein f
24	1685	100.0	317	8	ADM96241	Adm96241 Human rec
25	1685	100.0	317	8	ADT08155	Adt08155 Human RAN
26	1685	100.0	317	8	ADU06570	Adu06570 Novel bro
27	1685	100.0	317	9	ADW09029	Adw09029 Human rec
28	1685	100.0	317	9	ADY16469	Ady16469 PRO polyp
29	1685	100.0	317	9	ADY74714	Ady74714 Human rec
30	1685	100.0	317	9	ADZ12661	Adz12661 Human can
31	1685	100.0	317	9	ADY97756	Ady97756 Human RAN
32	1677	99.5	317	2	AAW83018	Aaw83018 Osteoclas
33	1685	100.0	317	5	ADR29338	Adr29338 Mouse RAN
34	1424.5	84.5	316	8	ADT08153	Adt08153 Murine RA
35	1424.5	84.5	270	7	ADJ82113	Adj82113 Protein f
36	1422	84.4	316	2	AAW83017	Aaw83017 Osteoclas
37	1417.5	84.1	316	2	AAW83194	Aaw83194 Human ost
38	1417.5	84.1	316	2	AAW59654	Aaw59654 Amino aci
39	1417.5	84.1	316	2	AAY17874	Aay17874 Murine TR
40	1417.5	84.1	316	3	AAY91024	Aay91024 Mouse OBM
41	1417.5	84.1	316	3	AAY84418	Aay84418 Amino aci
42	1417.5	84.1	316	3	AAY84419	Aay84419 Amino aci
43	1417.5	84.1	316	5	AAU78289	Aau78289 Mouse TRA
44	1417.5	84.1	316	6	ABR42071	Abr42071 Human RAN
45	1417.5	84.1	316	6	ABB99477	Abb99477 Amino aci

ALIGNMENTS

RESULT 1
AAW83195

ID   AAW83195 standard; protein; 317 AA.
XX
AC   AAW83195;
XX
DT   11-FEB-1999 (first entry)
XX
DE   Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.insert.
XX
KW   Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
KW   osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW   hypercalcaemia; osteoclast differentiation and activation receptor;
KW   Paget's disease.
XX
OS   Homo sapiens.
XX
PN   WO9846751-A1.
XX
PD   22-OCT-1998.
XX
PF   15-APR-1998; 98WO-US007584.
XX
PR   16-APR-1997; 97US-00842842.
PR   23-JUN-1997; 97US-00880855.
PR   30-MAR-1998; 98US-00052521.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ;
XX
DR   WPI; 1998-594578/50.
DR   N-PSDB; AAV70285.
XX
PT   Nucleic acid encoding osteoprotegerin binding protein - useful for, e.g.
PT   treating bone diseases by modulating osteoclast differentiation and for
PT   diagnosis.
XX
PS   Claim 19; Fig 4; 47pp; English.
XX
CC   The present sequence is human osteoprotegerin (OPG) binding protein. Host
CC   cells transfected with vectors containing nucleic acid molecules encoding
CC   OPG binding protein are used to produce recombinant OPG binding protein.
CC   OPG binding protein is used in binding assays to determine osteoprotegerin
CC   (OG) in biological samples; to screen for specific binding agents
CC   (particularly agonists and antagonists, including intracellular proteins)
CC   ; to raise Ab (useful in immunoassays for detection of OPG binding

CC   protein) and to identify compounds that module binding of OPG binding
CC   protein to osteoclast differentiation and activation receptor (ODAR). The
CC   nucleic acid molecule encoding OPG binding protein can be used to detect
CC   OPG binding protein-encoding sequences, e.g. screening for related
CC   sequences, also to produce transgenic animal models, while complementary
CC   sequences are used for antisense regulation of OPG binding protein
CC   expression. Modulators of OPG binding protein, particularly soluble forms
CC   of OPG binding protein or Ab, are used to treat or prevent bone diseases,
CC   e.g. osteoporosis, bone loss caused by arthritis or metastases,
CC   hypercalcaemia, Paget's disease, periodontal disease, osteoporosis,
CC   loosening of prostheses, optionally in combination with agents that
CC   promote bone growth
XX
SQ   Sequence 317 AA;

Query Match   100.0%; Score 1685; DB 2; Length 317;
Best Local Similarity   100.0%; Pred. No. 7.5e-154;
Matches 317;   Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 QAFQGAVQKELQHIVSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
         |||||||||||||||||
Db 301 PDQDATYFGAFKVRDID 317

RESULT 2
AAW69957
ID   AAW69957 standard; protein; 317 AA.
XX
AC   AAW69957;
XX
DT   08-OCT-1998 (first entry)
XX
DE   NF-kB receptor activator RANK ligand (RANKL).
XX
KW   RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW   immune response; inflammatory response; toxic shock; sepsis; RANKL;
KW   RANK ligand; tumour necrosis factor; TNF.
XX
OS   Homo sapiens.
XX
PN   WO9828426-A2.
XX
PD   02-JUL-1998.
XX
PF   22-DEC-1997; 97WO-US023775.
XX
PR   23-DEC-1996; 96US-0059978P.
PR   07-MAR-1997; 97US-0081350P9.
PR   14-OCT-1997; 97US-0064671P.
XX
PA   (IMMV) IMMUNEX CORP.
XX
PI   Anderson DM, Galibert LJ, Maraskovsky E;

XX
DR   WPI; 1998-377657/32.
DR   N-PSDB; AAV41378.
XX
PT   New isolated ligand for receptor activator of NF-kappa B - used to
PT   develop products for augmenting an immune response for inhibiting an
PT   inflammatory response and for protection of cells.
XX
PS   Claim 27; Page 59-60; 80pp; English.
XX
CC   This represents a human RANKL, a ligand for the RANK (receptor activator
CC   of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the
CC   tumour necrosis factor (TNF) family. A soluble RANK may be used for
CC   inhibiting activation of NF-kB, by contacting a cell expressing membrane-
CC   associated RANK with a soluble RANK which binds to RANK ligand (RANKL).
CC   RANKL polypeptides can activate RANK and can be used to induce maturation
CC   of dendritic cells and enhance their allo-stimulatory capacity, thereby
CC   augmenting an immune response. The soluble RANK polypeptide composition
CC   may also be used for regulating an immune or inflammatory response.
CC   Inhibition of NF-kB by RANK antagonists may be useful in ameliorating
CC   negative effects of an inflammatory response that result from triggering
CC   of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host
CC   reactions, or acute inflammatory reactions. They can also be used in
CC   adjunct therapy for disease characterised by neoplastic cells that
CC   express RANK. RANKL polypeptides can also be used to identify inhibitors
CC   of RANK and thus inhibitors of an inflammatory response, and also for
CC   protecting RANK-expressing cells from the negative effects of
CC   chemotherapy or the presence of high levels of TNF-alpha. The products
CC   can also be used for detection and drug screening
XX
SQ   Sequence 317 AA;

Query Match   100.0%; Score 1685; DB 2; Length 317;
Best Local Similarity   100.0%; Pred. No. 7.5e-154;
Matches 317;   Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 QAFQGAVQKELQHIVSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
         |||||||||||||||||
Db 301 PDQDATYFGAFKVRDID 317

RESULT 3
AAW68293
ID   AAW68293 standard; protein; 317 AA.
XX
AC   AAW68293;
XX
DT   08-OCT-1998 (first entry)
XX
DE   NF-kB receptor activator RANK ligand (RANKL).
XX
KW   RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW   immune response; inflammatory response; toxic shock; sepsis; RANKL;

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: December 21, 2005, 12:47:51 ; Search time 35.8574 Seconds
(without alignments)
850.612 Million cell updates/sec

Title: US-09-211-297-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.............LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62.
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621676 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   PIR_80:*
          1: pir1:*
          2: pir2:*
          3: pir3:*
          4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	189	11.2	281	2	I38707	Fas ligand - human
2	184.5	10.9	279	2	A53062	Fas ligand - mouse
3	176.5	10.5	261	2	S53090	CD40 ligand - bovi
4	175.5	10.4	278	2	A49266	fas ligand - rat
5	158.5	9.4	261	2	I53476	CD40 ligand - huma
6	141.5	8.4	235	1	QWMSN	tumor necrosis fac
7	141	8.4	235	1	A25451	tumor necrosis fac
8	137	8.1	234	1	JH0529	tumor necrosis fac
9	133	7.9	233	1	QWHUN	tumor necrosis fac
10	132.5	7.9	235	2	S54490	tumor necrosis fac
11	131.5	7.8	235	2	JU0029	lymphotoxin-beta -
12	130.5	7.7	306	2	I49139	tumor necrosis fac
13	130	7.7	233	1	S22052	tumor necrosis fac
14	128	7.6	234	1	JQ1344	tumor necrosis fac
15	126.5	7.5	233	1	S24642	tumor necrosis fac
16	126	7.5	232	1	S12606	tumor necrosis fac
17	125.5	7.4	185	2	S52715	tumor necrosis fac
18	122	7.2	193	2	S06192	tumor necrosis fac
19	120	7.1	260	2	S21738	tumor necrosis fac
20	117	6.9	233	2	S11688	tumor necrosis fac
21	117	6.9	244	2	A46066	lymphotoxin beta
22	97.5	5.8	1464	1	CGHU1S	collagen alpha 1(I
23	94.5	5.6	664	2	C84747	probable protein k
24	92.5	5.5	205	1	QWHUX	lymphotoxin alpha
25	92.5	5.5	450	2	S38114	hypothetical prote
26	91.5	5.4	3848	2	T17414	TipC protein - sli
27	91	5.4	493	2	AC0937	probable GntR-fami
28	90.5	5.4	1694	2	S50065	sialoadhesin - mou
29	90	5.3	730	2	JC1456	gelatinase B (EC 3
30	89.5	5.3	331	2	AF3526	homoprotocatechuat
31	89.5	5.3	379	2	A47659	farnesyl-protein t
32	89	5.3	202	1	B27303	tumor necrosis fac
33	89	5.3	440	2	I49681	glyceraldehyde-3-p
34	89	5.3	479	2	A25052	fibrinogen beta ch
35	89	5.3	639	2	C83624	probable two-compo
36	88.5	5.3	565	2	C89893	hypothetical prote
37	88.5	5.3	578	2	S51379	probable phosphoes
38	88.5	5.3	684	2	T01267	leucine-rich repea
39	88.5	5.3	883	2	A47733	[heparan sulfate] -
40	87.5	5.2	610	2	T06690	galactonolactone d
41	87.5	5.2	1466	1	CGHU1L	collagen alpha 1(I
42	87	5.2	639	2	A32935	protein P1 - Entam
43	87	5.2	1114	2	JH0284	125K surface antig
44	87	5.2	1315	2	G96722	hypothetical prote
45	86.5	5.1	279	2	F72339	hypothetical prote

ALIGNMENTS

RESULT 1
I38707
Fas ligand - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38707; JC2340; S57565; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.
A;Reference number: I38707; MUID:95127560; PMID:7826947
A;Accession: I38707
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: UNIPARC:UPI0000000D91A; GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA
R;Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A;Accession: S57565
A;Molecule type: mRNA
A;Status: preliminary
A;Accession: S57565
A;Residues: 1-281 <RES>
A;Cross-references: UNIPROT:P48023; UNIPARC:UPI0000000D91A; EMBL:U11821; NID:g559430; PID
R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.;
Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Accession: JC2340
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: UNIPARC:UPI0000000D91A; EMBL:X89102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-281 <RE2>
A;Cross-references: UNIPARC:UPI0000000D91A; EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PI
A;Genetic:
C;Genetic:
A;Gene: FasL
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.2%; Score 189; DB 2; Length 281;
Best Local Similarity 21.7%; Pred. No. 2e-08;
Matches 69; Conservative 43; Mismatches 98; Indels 108; Gaps 11;

Qy   22 PGAPHEGPLHAPPPPAP----HQPPAASRS---------------MFVALLGLGLGQVVCS 63

RESULT 2
A53062
Fas ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A53062
R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A;Reference number: A53062; MUID:94185175; PMID:7511063
A;Accession: A53062
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-279 <TAK>
A;Cross-references: UNIPROT:P41047; UNIPARC:UPI00000004022; GB:U06948; NID:g473564; PIDN:

Query Match   10.9%;   Score 184.5; DB 2; Length 279;
Best Local Similarity 21.7%; Pred. No. 4.9e-08;
Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps 11;

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Qy   13 RGSEEMGGGPGAPHEGPLHAPPPPAPHQP------------------------------PAASRSMFVALLGLGL 57
            :|:|  |: ||  | |  |::|                                  |:||||:|:|:
Db   38 RGPDQRPPPPPPPPPVSPLPPPSQPLPLPTPLKKDHNTNLWLPVVFFMVLVALVGMGL 97

Qy   58 GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLRHENADFQDTTLLESQDTKLIPDSCR 117
Db   98 G---------MYQLFHL----------------------------------------- 105

Qy  118 RIKQAFQGAVQKELQHI---VGSQHIRA----EKAMVDGSWLDLAKRSKLEAQPFAHLTINA 172
Db  106 -QKELAELREFTNQSLKYSSFEKQIANPS----TPSEKKEPRSVAHLTGN- 150

Qy  173 TDIPSGSHKVSLS-SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
Db  151 -----PHSRIPLEWEDTYGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQSCN-- 201

Qy  232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISI 291
Db  202 -NQPLNHKVYMRNS--KYPEDLVIMEEKRLNYCT-TGQIWAHSSYLGAVFNLTSADHLYV 257

Qy  292 EVSNPSLLDPDQDATYFGAFKV 313
Db  258 NISQLSLINFEESKTFFGLYKL 279
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RESULT 3
S53090
CD40 ligand - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S53090
R;Mertens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: S53090
A;Accession: S53090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <MER>
A;Cross-references: UNIPROT:P51749; UNIPARC:UPI00001370a9; EMBL:Z48469; NID:g732569; PID

Query Match   10.5%;   Score 176.5; DB 2; Length 261;
Best Local Similarity 24.2%; Pred. No. 2.1e-07;
Matches 70; Conservative 54; Mismatches 122; Indels 43; Gaps 13;

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Qy   33 PPPPAPHQPPAASRSMFVALLGLGL-GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRIL 91
Db    8 PSPRSVATGPPVSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-------R 57

Qy   92 RLHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDG 149
Db   58 NLHEDFVFMKITQRCNKGEGSLSLINCEEIRSRFEDLVKDIMQ----NKEVKKEKNFE- 112

Qy  150 SWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-L 206
Db  113 -----MHKGDQEPQIAAHVISEAS-----SKTTSVLQW-APKGYYTLSNNLVTLENGKQL 161

Qy  207 IVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIP--SSHTLMKGGSTKYW 264
Db  162 AVKRQGFYYIYTQVTFCSNR-------ETLSQAPFIASLCLKSPSGSERILLRAANTH-- 212

Qy  265 SGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
Db  213 SSSKPCCQQSIHLGGVFELQSGASVFVNVTDPSQVSHGTGFTSFGLLKL 261
```

RESULT 4
A49266
fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
A;Cross-references: UNIPROT:P36940; UNIPARC:UPI0000137085; GB:U03470; NID:g440178; PIDN:
C;Keywords: glycoprotein; transmembrane protein

Query Match   10.4%;   Score 175.5; DB 2; Length 278;
Best Local Similarity 20.3%; Pred. No. 2.8e-07;
Matches 64; Conservative 47; Mismatches 106; Indels 99; Gaps 10;

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Qy   21 GPGAPHEGPLHAPPPPAPHQPPAASRSM--------------------------------FVALLGLGL 57
Db   39 GPGQRPPP--PPPPPSPLPPPSQPPLPLSPLPKKDNIELWLPVIFFMVLVALVGMGL 96

Qy   58 GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLRHENADFQDTTLLESQDTKLIPDSCR 117
Db   97 G---------MYQLFHLQKELAELREFTNHSL-RVSSFEKQIANPSTPSETKKPRSV---- 143

Qy  118 RIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPS 177
Db  144 ------------------------------------------------AHLTGNPR---- 151

Qy  178 GSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQ 237
Db  152 -SRSIPL-EWEDTYGTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQSCN---SQPLS 205
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(continuation of RESULT 1 alignment)

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Db   46 PPPPPPLPPPPPPPPPLPLPLPLPPLPKRGNHSTGLCLLVMFPMVLVALVGLGIG----- 100
Db   64 VALFFYFRAQMDPNRISEDGTHCIYRIRLRHENADFQDTTLLESQDTKLIPDSCRRIKQAF 123
Db  101 -MFQLFHLQ------------------------------------KELAELRESTSQMTA- 124
Db  124 QGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLT--INATDIPSGSHK 181
Db  125 -SSLEKQIGH--------------------------PSPPEKKELRKVAHLTGKSNSRSMP---- 159
Db  182 VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVY 241
Db  160 ---LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNN-----------LPLSHK 210
Db  242 VTKTSIKIPSSHTLMKGGSTKY-----------WSGNSEFHFYSINVGGFFKLRSGEEISIEVSN 295
Db  211 VYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSS------------YLGAVFNLTSADHLYVNVSE 263
Qy  296 PSLLDPDQDATYFGAFKV 313
Db  264 LSLVNFEESQTFFGLYKL 281
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 13:02:07 ; Search time 174.61 Seconds (without alignments)
758.559 Million cell updates/sec

Title: US-09-211-297-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.........LLDPDQDATYFGAFKVRDID 317
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Match Length	DB	ID	Description
1	1685	100.0	317	3	US-09-813-329-7	Sequence 7, Appli
2	1685	100.0	317	3	US-09-871-856-13	Sequence 13, Appli
3	1685	100.0	317	3	US-09-957-944-6	Sequence 6, Appli
4	1685	100.0	317	3	US-09-865-363-13	Sequence 13, Appl
5	1685	100.0	317	3	US-09-871-291-13	Sequence 13, Appl
6	1685	100.0	317	3	US-09-877-650-13	Sequence 13, Appl
7	1685	100.0	317	3	US-09-933-915A-2	Sequence 10, Appli
8	1685	100.0	317	3	US-09-151-071-10	Sequence 22, Appli
9	1685	100.0	317	4	US-10-218-547-22	Sequence 22, Appl
10	1685	100.0	317	4	US-10-405-878-11	Sequence 11, Appl
11	1685	100.0	317	4	US-10-167-182-11	Sequence 11, Appl
12	1685	100.0	317	4	US-10-310-793-28	Sequence 28, Appl
13	1685	100.0	317	4	US-10-460-623-11	Sequence 11, Appl
14	1685	100.0	317	4	US-10-289-456-79	Sequence 79, Appl
15	1685	100.0	317	4	US-10-202-062-22	Sequence 22, Appl
16	1685	100.0	317	4	US-10-664-801-2	Sequence 2, Appli
17	1685	100.0	317	4	US-10-381-160-6	Sequence 6, Appli
18	1685	100.0	317	4	US-10-799-345-12	Sequence 12, Appli
19	1685	100.0	317	4	US-10-399-116-6	Sequence 6, Appli
20	1685	100.0	317	5	US-10-802-133-13	Sequence 13, Appli
21	1685	100.0	317	5	US-10-825-898-4	Sequence 4, Appli
22	1685	100.0	317	5	US-10-854-300-11	Sequence 11, Appl
23	1685	100.0	317	5	US-10-129-595-1	Sequence 1, Appli
24	1685	100.0	317	5	US-10-451-200-6	Sequence 6, Appli
25	1685	100.0	317	5	US-10-999-523-8	Sequence 8, Appli
26	1685	100.0	317	5	US-11-028-780-22	Sequence 22, Appli
27	1685	100.0	317	6	US-11-099-059-6	Sequence 6, Appli
28	1685	100.0	317	6	US-11-135-521-11	Sequence 11, Appl
29	1685	100.0	317	6	US-11-142-736-7	Sequence 7, Appli
30	1424.5	84.5	316	3	US-09-957-944-8	Sequence 8, Appli
31	1424.5	84.5	316	3	US-10-799-345-10	Sequence 10, Appli
32	1422	84.4	270	4	US-10-289-456-80	Sequence 80, Appli
33	1422	84.4	316	3	US-09-079-569-7	Sequence 7, Appli
34	1417.5	84.1	316	3	US-09-873-829-4	Sequence 4, Appli
35	1417.5	84.1	316	3	US-09-933-915A-16	Sequence 16, Appl
36	1417.5	84.1	316	4	US-10-017-910-4	Sequence 4, Appli
37	1417.5	84.1	316	4	US-10-105-057-2	Sequence 2, Appli
38	1417.5	84.1	316	4	US-10-272-411-19	Sequence 19, Appli
39	1417.5	84.1	316	4	US-10-326-052-2	Sequence 2, Appli
40	1417.5	84.1	316	4	US-10-272-328A-19	Sequence 19, Appl
41	1417.5	84.1	316	4	US-10-167-182-1	Sequence 1, Appli
42	1417.5	84.1	316	4	US-10-460-623-1	Sequence 1, Appli
43	1417.5	84.1	316	4	US-10-664-801-4	Sequence 4, Appli
44	1417.5	84.1	316	4	US-10-664-801-6	Sequence 6, Appli
45	1417.5	84.1	316	4	US-10-664-801-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-813-329-7
; Sequence 7, Application US/09811329
; Patent No. US2002012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Suibb Company
; TITLE OF INVENTION: No. US2002012968A1e1 Drosophila Tumor Necrosis Factor Class Mole
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-7

Query Match   100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity   100.0%; Pred. No. 4.9e-149;
Matches 317; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRRASRDYTKYLRGSEEMGGGPGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Db   1 MRRASRDYTKYLRGSEEMGGGPGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy   121 QAFQGAVQKELQHIVSSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 QAFQGAVQKELQHIVSSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy   181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy   241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy   301 PDQDATYFGAFKVRDID 317
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Db   301 PDQDATYFGAFKVRDID 317

RESULT 2
US-09-871-856-13
; Sequence 13, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; MaraskovSky, Eugene
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-856-13

Query Match   100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.9e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MRRASRDYTKYLRGSEEMCGGPGCAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Qy   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy  121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
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Db  121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy  181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICRHHETSGDLATEYLQLMV 240

Qy  241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy  301 PQDDATYFGAFKVRDID 317
        |||||||||||||||||
Db  301 PQDDATYFGAFKVRDID 317
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RESULT 3
US-09-957-944-6
; Sequence 6, Application US/09957944
; Publication No. US20020086312A1
; GENERAL INFORMATION:
; APPLICANT: Dougall, William C.
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS AND ANTAGONISTS OF RECEPTOR ACTIVAT
; TITLE OF INVENTION: NF-kappa B
; FILE REFERENCE: 3109-A
; CURRENT APPLICATION NUMBER: US/09/957,944
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/235,157
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-944-6

Query Match   100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.9e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MRRASRDYTKYLRGSEEMCGGPGCAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRRASRDYTKYLRGSEEMCGGPGCAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy  121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy  181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICRHHETSGDLATEYLQLMV 240

Qy  241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy  301 PQDDATYFGAFKVRDID 317
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Db  301 PQDDATYFGAFKVRDID 317
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RESULT 4
US-09-865-363-13
; Sequence 13, Application US/09865363
; Publication No. US20020086826A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; COMPUTER READABLE FORM:

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                                 GenCore version 5.1.6

                                 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:          December 21, 2005, 13:03:52 ; Search time 9.87377 Seconds
                                           (without alignments)
                                 228.978 Million cell updates/sec

Title:           1685
Perfect score:   1685
Sequence:        1 MRRASRDYTKYLRGSEEMGG..........LLDPDQDATYFGAFKVRDID 317

Scoring table:   BLOSUM62
Scoring table:   Gapop 10.0 , Gapext 0.5

Searched:        53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters:     53982

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA_New:*
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           2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
           3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
           4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
           5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
           6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
           7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
           8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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Result                   %
No.    Score   Query  Match  Length  DB  ID                   Description
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  1    538     31.9    7     109     US-11-065-669-8           Sequence 8, Appli
  2    251.5   14.9    7     281     US-10-821-234-1288        Sequence 1288, Ap
  3    247.5   14.7    7     281     US-11-077-272-2           Sequence 2, Appli
  4    235.5   14.0    7     266     US-11-082-544-10          Sequence 10, Appl
  5    232.5   13.8    7     391     US-11-105-172-4           Sequence 4, Appli
  6    147.5    8.8    7     359     US-11-105-172-2           Sequence 2, Appli
  7    134      8.0    6     240     US-10-987-663-6           Sequence 6, Appl
  8    133      7.9    7     157     US-11-010-954-1           Sequence 1, Appli
  9    133      7.9    7     157     US-11-053-750-1           Sequence 1, Appli
 10    133      7.9    7     157     US-11-053-749-1           Sequence 1, Appli
 11    133      7.9    7     157     US-11-108-001-12          Sequence 12, Appl
 12    133      7.9    7     158     US-11-082-544-4           Sequence 4, Appli
 13    133      7.9    7     164     US-11-108-001-2           Sequence 2, Appli
 14    133      7.9    7     180     US-11-082-544-8           Sequence 8, Appli
 15     99.5    5.9    6     438     US-10-821-234-1051        Sequence 1051, Ap
 16     97.5    5.8    6     438     US-11-186-284-28          Sequence 28, Appl
 17     97      5.8    7     1464    US-11-000-463-243         Sequence 243, App
 18     97      5.8    6     1467    US-11-234-234-1096        Sequence 1096, Ap
 19     96.5    5.7    6     371     US-10-995-561-572         Sequence 572, App
 20     92.5    5.5    7     177     US-10-999-866-61          Sequence 61, Appl
 21     92.5    5.5    6     205     US-10-995-561-1028        Sequence 1028, Ap
 22     92.5    5.5    6     205     US-11-140-417-1           Sequence 1029, Ap
 23     90      5.3    7     432     US-11-140-417-2           Sequence 4, Appli
 24     89      5.3    7     438     US-11-140-417-2           Sequence 2, Appli
 25     88.5    5.3    7     1163    US-11-044-899-2           Sequence 2, Appli
 26     88.5    5.3    7     1163    US-11-044-899-30          Sequence 30, Appl
 27     87.5    5.2    6     610     US-10-606-302-1           Sequence 1, Appli
 28     86.5    5.1    6     104     US-11-065-669-5           Sequence 5, Appli
 29     86.5    5.1    7     1166    US-10-821-234-964         Sequence 964, Appl
 30     86.5    5.1    6     1466    US-11-186-284-33          Sequence 33, Appl
 31     85      5.0    7     220     US-11-054-515-3233        Sequence 3233, Ap
 32     81.5    4.8    7     239     US-11-054-515-3232        Sequence 3232, Ap
 33     81      4.8    6     484     US-11-821-234-933         Sequence 933, App
 34     79.5    4.7    6     903     US-11-057-058-65          Sequence 65, Appl
 35     79.5    4.7    6     1001    US-10-467-962b-81         Sequence 81, Appl
 36     79      4.7    6     453     US-11-234-234-1185        Sequence 1185, Ap
 37     79      4.7    6     457     US-10-131-826A-270        Sequence 270, App
 38     78.5    4.6    7     400     US-11-054-515-3231        Sequence 3231, Ap
 39     77.5    4.6    6     290     US-11-186-284-155         Sequence 155, App
 40     77      4.6    7     200     US-10-524-198-2           Sequence 2, Appli
 41     77      4.6    6     285     US-11-054-515-3231        Sequence 2, Appli
 42     77      4.6    6     285     US-11-131-826A-24         Sequence 24, Appli
 43     77      4.6    6     285     US-10-742-634-2           Sequence 1, Appli
 44     77      4.6    7     285     US-11-065-669-1           Sequence 2, Appli
 45     76.5    4.5    7     219     US-11-054-515-3228        Sequence 1, Appli
                                     US-11-054-515-3228        Sequence 3228, Ap
                                     US-11-054-515-3237        Sequence 3237, Ap
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ALIGNMENTS

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RESULT 1
US-11-065-669-8
; Sequence 8, Application US/11065669
; Publication No. US20050244411A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Kalled, Susan
; TITLE OF INVENTION: BAFF, INHIBITORS THEREOF AND THEIR USE IN THE
; TITLE OF INVENTION: MODULATION OF B-CELL RESPONSE
; FILE REFERENCE: 08201.0024-04000
; CURRENT APPLICATION NUMBER: US/11/065,669
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 10/045,574
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/911,777
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/143,228
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-065-669-8

  Query Match             31.9%;  Score 538;  DB 7;  Length 109;
  Best Local Similarity   75.5%;  Pred. No. 5.9e-44;
  Matches  108;  Conservative    0;  Mismatches   1;  Indels   34;  Gaps   2;

Qy    161 EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQGFYYLYANI 220
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Db      1 EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWGKISNM--------------YANI 43

Qy    221 CFRHHETSGDLATEYLQLMVYVTKISIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGF 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     44 CFRHHETSGDLATEYLQLMVVVTKTSIKIP------------------SEFHFYSINVGGF 86

Qy    281 FKLRSGEEISIEVSNPSLLDPDQ 303
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Db     87 FKLRSGEEISIEVSNPSLLDPDQ 109


RESULT 2
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US-10-821-234-1288
  Sequence 1288, Application US/10821234
  Publication No. US20050255114A1
  GENERAL INFORMATION:
  APPLICANT: Labat, Ivan
  APPLICANT: Stache-Crain, Birgit
  APPLICANT: Andarmani, Susan
  APPLICANT: Tang, Y. Tom
  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
  FILE REFERENCE: 821A
  CURRENT APPLICATION NUMBER: US/10/821,234
  CURRENT FILING DATE: 2004-04-07
  PRIOR APPLICATION NUMBER: US 60/462,047
  PRIOR FILING DATE: 2003-04-07
  NUMBER OF SEQ ID NOS: 1704
  SOFTWARE: pt_SEQ_genes Version 1.0
  SEQ ID NO 1288
  LENGTH: 281
  TYPE: PRT
  ORGANISM: Homo sapiens

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Best Local Similarity 24.1%; Pred. No. 1.7e-16;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

Qy  42 PAASRSMFVALLGLGLGQVVCSVALFPYPRAQMD--PNRISEDGTHCIYRILRLHENADF  99
Db  10 PSLGQTCVLIVIFVLLQSLCVAVTYVVFTNELKQMQDKYSKSGIACF-----LKED---  61

Qy 100 QDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSK 159
Db  62 -DSYWDPNDEESMNSPCWQVKW-------QLRQLVRKMILRTSEETI-----STVQEKQ 107

Qy 160 LEAQPF---------AHLT-----INATDIPSGSHKVSL----SSWYHDR-GWAKISNM 199
Db 108 QNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167

Qy 200 TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG 259
Db 168 HLRNGELVIHEKGFYYIYSQTYRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSA 226

Qy 260 STKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
Db 227 RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLV 280


RESULT 3
US-11-077-272-2
  Sequence 2, Application US/11077272
  Publication No.US20050244927A1
  GENERAL INFORMATION:
  APPLICANT: LEUNG, WOON-LAM SUSAN
  APPLICANT: SWARTZ, JAMES R.
  TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDES
  FILE REFERENCE: P2019R1
  CURRENT APPLICATION NUMBER: US/11/077,272
  CURRENT FILING DATE: 2005-03-10
  PRIOR APPLICATION NUMBER: US 60/552,678
  PRIOR FILING DATE: 2004-03-11
  NUMBER OF SEQ ID NOS: 7
  SEQ ID NO 2
  LENGTH: 281
  TYPE: PRT
  ORGANISM: Homo sapiens

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Best Local Similarity 24.1%; Pred. No. 4e-16;
Matches 71; Conservative 60; Mismatches 118; Indels 45; Gaps 10;

Qy  42 PAASRSMFVALLGLGLGQVVCSVALFPYPRAQMD--PNRISEDGTHCIYRILRLHENADF  99
Db  10 PSLGQTCVLIVIFVLLQSLCVAVTYVVFTNELKQMQDKYSKSGIACF-----LKED---  61

Qy 100 QDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSK 159
Db  62 -DSYWDPNDEESMNSPCWQVKW-------QLRQLVRKMILRTSEETI-----STVQEKQ 107

Qy 160 LEAQPF---------AHLT-----INATDIPSGSHKVSL----SSWYHDR-GWAKISNM 199
Db 108 QNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167

Qy 200 TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG 259
Db 168 HLRNGELVIHEKGFYYIYSQTYRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSA 226

Qy 260 STKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
Db 227 RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLV 280


RESULT 4
US-11-082-544-10
  Sequence 10, Application US/11082544
  Publication No. US20050249706A1
  GENERAL INFORMATION:
  APPLICANT: King, I.
  APPLICANT: Clairmont, C.
  APPLICANT: Lin, S.
  APPLICANT: Belcourt, M.
  APPLICANT: Bermudes, G.
  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
  TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
  FILE REFERENCE: 8002-059
  CURRENT APPLICATION NUMBER: US/11/082,544
  CURRENT FILING DATE: 2005-03-17
  PRIOR APPLICATION NUMBER: US/09/645,415
  PRIOR FILING DATE: 2000-08-24
  PRIOR APPLICATION NUMBER: 60/157,581
  PRIOR FILING DATE: 1999-10-04
  PRIOR APPLICATION NUMBER: 60/157,637
  PRIOR FILING DATE: 1999-10-04
  NUMBER OF SEQ ID NOS: 61
  SOFTWARE: FastSEQ for Windows Version 3.0
  SEQ ID NO 10
  LENGTH: 266
  TYPE: PRT
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Fusion construct
US-11-082-544-10

Query Match       14.0%; Score 235.5; DB 7; Length 266;
Best Local Similarity 25.3%; Pred. No. 5e-15;
Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;

Qy  77 NRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVG 136
Db  32 DKYSKSGIACF-----LKED----DSYWDPNDEESMNSPCWQVKW------QLRQLVR  74

Qy 137 SQHIRAEKAMVDGSWLDLAKRSKLEAQPF---------AHLT-----INATDIPSGGHK 181
Db  75 KMILRTSEETI-----STVQEKQONISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNE 129

Qy 182 VSL----SSWYHDR-GWAKISNMTFSNGKLIVNQDGFYYSINVGGFFKLRSGEEISIEVSNP 236
Db 130 KALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYRFQEEIKENTKNDK 189

Qy 237 QLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNP 296
Db 190 QMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNE 248

Qy 297 SLLDPDQDATYFGAFKV 313
Db 249 HLIDMDHEASFPGAFLV 265
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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 12:34:10 ; Search time 169.402 Seconds
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Perfect score: 1319
Sequence: 1 YFRAQMDNRISEDGTHCIY.........LLDPDQDATYFGAFKVRDID 249

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Database : US-09-211-297-39_COPY_69_317

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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 2: geneseqp1990s:*
 3: geneseqp2000b:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2002aa:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1319	100.0	249	5	ABG80594	Abg80594 Human rec
3	1319	100.0	249	7	ADJ82115	Adj82115 Protein f
4	1319	100.0	250	6	ADA50079	Adas0079 Human wil
5	1319	100.0	270	2	ADJ82113	Adj82113 Protein f
6	1319	100.0	317	2	AAW83018	Aaw83018 Osteoclas
7	1319	100.0	317	2	AAW83195	Aaw83195 Human ost
8	1319	100.0	317	2	AAW69957	Aaw69957 NF-kB rec
9	1319	100.0	317	2	AAW68293	Aaw68293 NF-kB rec
10	1319	100.0	317	2	AAE08738	Aae08738 Human rec
11	1319	100.0	317	4	AAY84417	Aay84417 Amino aci
12	1319	100.0	317	4	AAE04426	Aae04426 Human rec
13	1319	100.0	317	4	AAE01993	Aae01993 Human ful
14	1319	100.0	317	4	ABB08134	Abb08134 Human RAN
15	1319	100.0	317	5	AAE26103	Aae26103 Human RAN
16	1319	100.0	317	5	ABG31631	Abg31631 Human RAN
17	1319	100.0	317	5	AAU78285	Aau78285 Human TRA
18	1319	100.0	317	5	AAO19096	Aao19096 C neoform
19	1319	100.0	317	5	ADR29336	Adr29336 Human RAN
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21	1319	100.0	317	6	AAE34364	Aae34364 Human rec
22	1319	100.0	317	6	ABR42314	Abr42314 Human RAN
23	1319	100.0	317	7	ADB16988	Adb16988 Human RAN
24	1319	100.0	317	7	ADC35204	Adc35204 Human TNF
25	1319	100.0	317	7	ADC73002	Adc73002 Human RAN
26	1319	100.0	317	7	ADC78268	Adc78268 Human RAN
27	1319	100.0	317	7	ABW02277	Abw02277 Human RAN
28	1319	100.0	317	7	ADG46723	Adg46723 Human RAN
29	1319	100.0	317	7	ADJ82112	Adj82112 Protein f
30	1319	100.0	317	8	ADM96241	Adm96241 Human rec
31	1319	100.0	317	8	ADT08155	Adt08155 Human RAN
32	1319	100.0	317	8	ADU06570	Adu06570 Novel bro
33	1319	100.0	317	9	ADW09029	Adw09029 Human rec
34	1319	100.0	317	9	ADY16469	Ady16469 PRO polyp
35	1319	100.0	317	9	ADY74714	Ady74714 Human can
36	1319	100.0	317	9	ADZ12661	Adz12661 Human rec
37	1319	100.0	317	9	ADY97756	Ady97756 Human RAN
38	1316	99.8	317	6	ADA50102	Adas0102 Human RAN
39	1316	99.8	317	6	ADA50098	Adas0098 Human RAN
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41	1316	99.8	317	6	ADA50095	Adas0095 Human RAN
42	1316	99.8	317	6	ADA50101	Adas0101 Human RAN
43	1315	99.7	250	6	ADA50089	Adas0089 Human RAN
44	1315	99.7	250	6	ADA50086	Adas0086 Human RAN
45	1315	99.7	250	6	ADA50099	Adas0099 Human RAN

ALIGNMENTS

RESULT 1
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ID ABG94282 standard; protein; 249 AA.
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AC ABG94282;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human RANKL extracellular domain.
XX
KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW vaccine; infectious disease.
XX
OS Homo sapiens.
XX
XX
PN WO200256905-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-IB000166.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0285549P.
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0311045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
PI Piossek C;
XX
DR WPI; 2002-627351/67.
XX
PT Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Disclosure; Page 420; 441pp; English.
XX
CC This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organiser comprising
CC at least one first attachment site, where the organiser is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment

```
CC   site, where the antigen or antigenic determinant is amyloid beta peptide
CC   (Abeta1-42) or its fragment and where the second attachment site is
CC   selected from an attachment site not naturally occurring with the antigen
CC   or antigenic determinant and an attachment site naturally occurring with
CC   the antigen or antigenic determinant, where the second attachment site is
CC   capable of association through at least one non-peptide bond to the first
CC   attachment site and where the antigen or antigenic determinant and the
CC   scaffold interact through the association to form an ordered and
CC   repetitive antigen array. The invention also comprises a coat protein
CC   capable of forming a capsid which comprises mutant Qbeta coat proteins
CC   having an amino acid sequence selected from five amino acid sequences
CC   fully defined in the specification. The compounds of the invention may
CC   have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC   antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC   immunisation and as a vaccine. The present sequence represents a protein
CC   sequence used to create the compositions of the invention
XX
SQ   Sequence 249 AA;

Qy        Best Local Similarity   100.0%;
          Matches  249;   Conservative  0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy      1 YFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQ   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 YFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQ   60

Qy     61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY  120

Qy    121 HDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMYVVTKTSIK  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMYVVTKTSIK  180

Qy    181 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF  240

Qy    241 GAFKVRDID  249
          |||||||||
Db    241 GAFKVRDID  249

RESULT 2
ABG80594
ID   ABG80594 standard; protein; 249 AA.
XX
AC   ABG80594;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human receptor activator of NFKB ligand, RANKL, extracellular part.
XX
KW   Molecular antigen array; vaccine; antigen; antimicrobial;
KW   Molecular scaffold; amyloid beta; Abeta 1-42; influenza;
KW   Grave's disease; systemic lupus erythematosus; osteoporosis;
KW   graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
KW   inflammatory immune disease; myasthenia gravis; multiple sclerosis;
KW   adult respiratory distress syndrome; ARDS; Crohn's disease;
KW   allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW   angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
KW   rheumatoid arthritis; diabetes; infectious disease; factor Xa;
KW   enterokinase; cysteine-containing linker.
XX
OS   Homo sapiens.
XX
PN   WO200256907-A2.
XX
PD   25-JUL-2002.
XX
PF   21-JAN-2002; 2002WO-IB000168.
```

```
XX
PR   19-JAN-2001; 2001US-02623379P.
PR   04-MAY-2001; 2001US-0288549P.
PR   05-OCT-2001; 2001US-0326998P.
PR   07-NOV-2001; 2001US-0331045P.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA   (NOVS ) NOVARTIS PHARMA AG.
PA   (MAUR/) MAURER P.
PA   (LECH/) LECHNER F.
PA   (ORTM/) ORTMANN R.
PA   (LUEO/) LUEOEND R.
PA   (STAU/) STAUFENBIEL M.
PA   (FREY/) FREY P.
XX
PI   Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
PI   Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
XX
DR   WPI; 2002-636514/68.
XX
PT   Molecular antigen array used in the production of vaccines for infectious
PT   diseases.
XX
PS   Disclosure; Page 397; 418pp; English.
XX
CC   The invention relates to a composition comprising: (a) a non-natural
CC   molecular scaffold comprising: (i) a core particle selected from: (1) a
CC   core particle of a non-natural origin; and (2) a core particle of natural
CC   origin; and (ii) an organiser comprising at least one first attachment
CC   site, where the organiser is connected to the core particle by at least
CC   one covalent bond; (b) an antigen or antigenic determinant with at least
CC   one second attachment site, where the antigen or antigenic determinant is
CC   amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC   attachment site is selected from: (i) an attachment site not naturally
CC   occurring with the antigen or antigenic determinant; and (ii) an
CC   attachment site naturally occurring with the antigen or antigenic
CC   determinant, where the second attachment site is capable of association
CC   through at least one non-peptide bond to the first attachment site; and
CC   where the antigen or antigenic determinant and the scaffold interact
CC   through the association to form an ordered and repetitive antigen array.
CC   Also included is a process for producing a non-naturally occurring
CC   ordered and repetitive antigen array. The composition is used in
CC   immunisation and as a vaccine for diseases such as influenza, graft
CC   versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
CC   respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC   acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
CC   systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC   gravis, immunoproliferative disease lymphadenopathy, immunoblastic
CC   angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
CC   rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC   osteoporosis and infectious diseases. The present sequence is modified to
CC   for use in the array of the invention. The antigen is modified to possess
CC   or a cleavage site (enterokinase or factor Xa) and a Cysteine-
CC   or C-terminal linker peptide which serves as the attachment point to a
CC   virus like particle or bacterial protein (the scaffold protein)
XX
SQ   Sequence 249 AA;

Qy        Best Local Similarity   100.0%;
          Matches  249;   Conservative  0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy      1 YFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQ   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 YFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQ   60

Qy     61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY  120

Qy    121 HDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMYVVTKTSIK  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMYVVTKTSIK  180
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OM protein - protein search, using sw model

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                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:             December 21, 2005, 12:47:51 ; Search time 28.1656 Seconds
                                               (without alignments)
                                               850.612 Million cell updates/sec

Title:              US-09-211-297-39_COPY_69_317
Perfect score:      1319
Sequence:           1 YFRAQMDPNRISEDGTHCIY..............LLDPDQDATYFGAFKVRDID 249

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched:           283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:          283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:    Minimum Match 0%
                    Maximum Match 100%
                    Listing first 45 summaries

Database :          PIR_80:*
                    1: pir1:*
                    2: pir2:*
                    3: pir3:*
                    4: pir4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	157	11.9	261	2	S53090	CD40 ligand - bovi
2	157	11.9	279	2	A53062	Fas ligand - mouse
3	150	11.4	261	2	S53062	CD40 ligand - mouse
4	149.5	11.3	281	2	I53476	CD40 ligand - huma
5	144	10.9	278	2	I38707	Fas ligand - human
6	141.5	10.7	235	1	A49266	tumor necrosis fac
7	137	10.4	235	1	QWMSN	tumor necrosis fac
8	134.5	10.2	234	1	JH0529	tumor necrosis fac
9	133	10.1	233	1	A25451	tumor necrosis fac
10	132.5	10.1	233	1	QWHUN	tumor necrosis fac
11	131.5	10.0	235	2	I54490	tumor necrosis fac
12	131	10.0	235	2	JU0029	tumor necrosis fac
13	130.5	9.9	306	2	I49139	lymphotoxin-beta -
14	130	9.9	233	1	S22052	tumor necrosis fac
15	128	9.7	234	1	JQ1344	tumor necrosis fac
16	126.5	9.6	233	1	S24642	tumor necrosis fac
17	126	9.6	232	1	S12606	tumor necrosis fac
18	125.5	9.5	185	2	S52715	tumor necrosis fac
19	122	9.2	193	2	S06192	tumor necrosis fac
20	117	8.9	244	2	S11688	tumor necrosis fac
21	117	8.9	244	2	A46066	lymphotoxin beta -
22	102.5	7.8	260	2	S21738	CD40 ligand - mous
23	92.5	7.0	205	1	QWHUX	lymphotoxin alpha
24	92.5	7.0	450	2	S38114	hypothetical prote
25	89	6.7	202	1	B27303	hypothetical prote
26	88.5	6.7	578	2	C89893	tumor necrosis fac
27	88.5	6.7	578	2	S51379	hypothetical prote
28	87	6.6	639	2	A32935	probable phosphoes
29	87	6.6	1114	2	JH0284	protein P1 - Entam
30	86.5	6.6	279	2	F72339	125K surface antig
31	86	6.5	272	2	AC1090	hypothetical prote
32	85	6.4	1151	2	S03722	phage proteins hom
33	84.5	6.4	197	1	JH0309	DNA-directed DNA p
34	84.5	6.4	202	1	JN0869	tumor necrosis fac
35	84.5	6.4	397	2	G84461	tumor necrosis fac
36	84	6.4	409	2	G95307	hypothetical prote
37	84	6.4	486	2	C64765	arginine deiminase
38	83.5	6.3	290	2	B97963	yaiT protein homol
39	83.5	6.3	399	1	A26916	conserved hypothet
40	83.5	6.3	431	2	F83123	ribonucleoside-dip
41	83	6.3	2325	2	T15566	probable porin PA4
42	83	6.3	272	2	AB1454	hypothetical prote
43	83	6.3	333	2	T28466	phage protein homo
44	83	6.3	479	2	A25052	ribonucleoside-dip
45	83	6.3	3848	2	T17414	fibrinogen beta ch
	82	6.2	160	2	T17005	major allergen Mal

ALIGNMENTS

```
RESULT 1
S53090
CD40 ligand - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S53090
R;Mertens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: S53090
A;Residues: 1-261 <MER>
A;Cross-references: UNIPROT:P51749; UNIPARC:UPI000001370A9; EMBL:Z48469; NID:G732569; PIL

Query Match    57.1%;  Score 157;  DB 2;  Length 261;
Best Local Similarity    25.0%;  Pred. No. 2.8e-06;
Matches  57;  Conservative  43;  Mismatches  96;  Indels  32;  Gaps  10;

Qy     25 LHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGS  82
          |||:|    |  :|||:| ||  |  |  | | :| |  |:::|:  |   ||   : ||
Db     59 LHEDFVFMKIIQRCNKGEGSLSLLNCEEIRSRFEDLVKDIMQ---NKEVKKEKNFE--  112

Qy     83 WLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-LI  139
          |  |  : |: |||  | : |  ||:|||| || :||:|:|| ||: |  ||||| | |:
Db    113 ---MHKGDQEPQIAAHVISEAS-----SKTTSVLQW-APKGYYTLSNNLVTLENGKQLA  162

Qy    140 VNQDGFYLYLYANICRRHHETSGDLIATEYLQLMVYTKTSIKIP--SSHTLMKGGSTKYWS  197
          :||:| || |     : :| :|   ||| :|| : |||  || |  |||: |  |  || |
Db    163 VRQGFYYIYTQVTFCSNR------ETLSQAPFIASLCLKSPGGSERILLRAANTH--S  213

Qy    198 GNSEFHFYSINVGGFFKLRGGEEISIEVSNPSLLDPDQDATYFGAFKV  245
          ||::| |: : ||||| ||| :|| |  | :: || :| |  | | |:
Db    214 SSKPCCQQSIHLGGVFELQSGASVFNVTDPSQVSHGTGFTSFGLLKL  261

RESULT 2
A53062
Fas ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A53062
R;Takahashi, T.; Tanaka, M.; Branman, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A;Reference number: A53062; MUID:94185175; PMID:7511063
A;Accession: A53062
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-279 <TAK>
A;Cross-references: UNIPROT:P41047; UNIPARC:UPI00000004022; GB:U06948; NID:G473564; PIDN
```

RESULT 3
I53476
CD40 ligand - human
N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-2004
C;Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;
EMBO J. 11, 4313-4321, 1992
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for
A;Reference number: JH0793; MUID:93094757; PMID:1281209
A;Accession: JH0793
A;Molecule type: mRNA
A;Residues: 1-261 <HOL>
A;Cross-references: UNIPARC:UPI000000315E7; UNIPROT:P29965; EMBL:Z15017; NID:g38483; PIDN
R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
J. Exp. Med. 176, 1543-1550, 1992
A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobuli
A;Reference number: S26694; MUID:93076854; PMID:1280226
A;Accession: S26694
A;Molecule type: mRNA
A;Residues: 1-261 <SPR>
A;Cross-references: UNIPARC:UPI000000315E7; GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g
R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczek, R.A.
Eur. J. Immunol. 22, 3191-3194, 1992
A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A;Reference number: S28852; MUID:93118085; PMID:7678552
A;Accession: S28852
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <GRA>
A;Cross-references: UNIPARC:UPI000000315E7; EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PI
R;Gauchat, J.F.; Aubry, J.P.; Mazzel, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.
FEBS Lett. 315, 259-266, 1993
A;Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e
A;Reference number: S28852
A;Accession: S28852
A;Molecule type: mRNA
A;Residues: 1-261 <GAU>
A;Cross-references: UNIPARC:UPI000000315E7; EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
C;Genetics:
A;Gene: GDB:CD40LG; HIGM1; IMD3
A;Cross-references: GDB:120632; OMIM:308230
A;Map position: Xq26-Xq26
C;Keywords: glycoprotein; transmembrane protein
F;13-44/Domain: transmembrane #status predicted <TMM>
F;45-261/Domain: extracellular #status predicted <EXT>
F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Query Match       11.9%; Score 157; DB 2; Length 279;
Best Local Similarity  25.9%; Pred. No. 3e-06;
Matches 50; Conservative 38; Mismatches 81; Indels 24; Gaps 8;

Qy  59 VQKELQHI--VGSQHIRA---EKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHK 113
Db 105 LQKELAELREFTNQSLKVSSFEKQIANPS----TPSEKKEPRSVAHLTGN------PHS 153
Qy 114 VSLS-SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 172
Db 154 RSIPLEWEDTYGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQSCN----NQPLNHKV 209
Qy 173 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 232
Db 210 YMRNS--KYPEDLVLMEEKRLNYCT-TGOIWAHSSYLGAVFNLTSADHLYVNISQLSIIN 266
Qy 233 PDDDATYFGAFKV 245
Db 267 FEESKTFFGLYKL 279
```

RESULT 4
I38707
Fas ligand - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38707; JC2340; S57565; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.
A;Reference number: I38707; MUID:95127560; PMID:7826947
A;Accession: I38707
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RES>
A;Cross-references: UNIPARC:UPI00000000D91A; UNIPROT:P48023; EMBL:U11821; NID:g595430; PID
R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.;
Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Accession: JC2340
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: UNIPARC:UPI00000000D91A; GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA
R;Schatzlein, C.B.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: UNIPARC:UPI00000000D91A; EMBL:X89102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Go
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: UNIPARC:UPI00000000D91A; EMBL:U08137; NID:g924627; PIDN:AAC50071.1; PI
C;Genetics:
A;Gene: FasL
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match       11.4%; Score 150; DB 2; Length 261;
Best Local Similarity  25.4%; Pred. No. 1.1e-05;
Matches 58; Conservative 43; Mismatches 95; Indels 32; Gaps 12;

Qy  25 LHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGS 82
Db  59 LHEDFVFMKTIQRCNTGERSLSLLNCEEIKSQPEGFV-KDIM------LNKEETKEENS 110
Qy  83 WLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-LI 139
Db 111 F-EMQKGDQ-NPQIAAHVISEAS-----SKTTSVLQW-AEKGYYTMSNNLVTLENGKQLT 162
Qy 140 VNQDGFYYLYANICFRHHETSGDLATEYLQLMYVTKTSIKIPS--SHTLMKGGSTKYWS 197
Db 163 VKRQGLYYIYAQVTFCSNREASSQAP------FIASLCLKSPGRFERILLRAANTH--S 213
Qy 198 GNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDDPPQDATYFGAFKV 245
Db 214 SAKPCGQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTFGTSFGLLKL 261
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```
Query Match       11.3%; Score 149.5; DB 2; Length 281;
Best Local Similarity  23.9%; Pred. No. 1.4e-05;
Matches 47; Conservative 33; Mismatches 74; Indels 43; Gaps 6;

Qy  71 HIRAEKAMVDGSWLDLAKRSKLEAQ-----------------PFAHLT--INATDIPSGSHKV 114
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                                              GenCore version 5.1.6

              Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:         December 21, 2005, 12:35:06 ; Search time 171.443 Seconds
                                              (without alignments)
                                              1024.696 Million cell updates/sec

Title:          US-09-211-297-39_COPY_69_317
Perfect score:  1319
Sequence:       1 YFRAQMDPNRISEDGTHCIY..........LLDPDQDATYFGAFKVRDID 249

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:    2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      UniProt_05.80:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
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SUMMARIES

```
Result                  %       Query
No.     Score       Match   Length  DB  ID              Description
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  1     1319  100.0    1     317    1   TNF11_HUMAN     O14788 h tumor nec
  2     1319  100.0    1     317    2   Q5T9Y4_HUMAN    Q5t9y4 homo sapien
  3     1292   98.0    1     244    2   Q54A98_HUMAN    Q54a98 homo sapien
  4     1127   85.4    1     316    1   TNF11_MOUSE     O35235 m tumor nec
  5     1118   84.8    1     318    1   TNF11_RAT       Q9ee2 r tumor nec
  6      482   36.5    2     290    2   Q5HZR8_XENLA    Q5hzr8 xenopus lae
  7      470   35.6    2     317    2   Q5XLH0_RABIT    Q5xlh0 oryctolagus
  8      253.5 19.2    2     317    2   Q7ZYX9_BRARE    Q7zyx9 brachydanio
  9      252.5 19.1    2     289    2   Q4VSR6_PIG      Q4vsr6 sus scrofa
 10      242   18.3    2     304    2   Q7T1F2_CHICK    Q7t1f2 gallus gall
 11      241.5 18.3    2     303    2   Q5XKN3_MOUSE    Q5xkn3 mus musculu
 12      240.5 18.2    2     214    2   Q9DDZ5_BRARE    Q9ddz5 brachydanio
 13      239.5 18.2    2     292    2   Q5ZK93_CHICK    Q5zk93 gallus gall
 14      238.5 18.1    1     291    1   TNF10_MOUSE     P50592 mus musculu
 15      238   18.0    2     299    2   Q4S9Q4_TETNG    Q4s9q4 tetraodon n
 16      237   18.0    2     299    2   Q6DHG9_BRARE    Q6dhg9 brachydanio
 17      236.5 17.9    1     281    1   TNF10_HUMAN     P50591 homo sapien
 18      236.5 17.9    2     281    2   Q6IBA9_HUMAN    Q6iba9 homo sapien
 19      219   16.6    2     300    2   Q5U675_HUMAN    Q5u675 homo sapien
 20      216.5 16.4    2     287    2   Q90WT9_CHICK    Q90wt9 gallus gall
 21      211   16.0    2     285    2   Q4SKU4_TETNG    Q4sku4 tetraodon n
 22      207.5 15.7    2     287    2   Q8K3G0_RAT      Q8k3g0 rattus norv
 23      184.5 14.0    2     252    2   Q8K3Y8_MOUSE    Q8k3y8 mus musculu
 24      181   13.7    2     252    2   Q6UWL7_HUMAN    Q6uwl7 homo sapien
 25      181   13.7    2      95    2   Q6UY13_HUMAN    Q6uy13 homo sapien
 26      179.5 13.6    2      95    2   Q80YZ0_MOUSE    Q80yz0 mus musculu
 27      177.5 13.5    2     252    2   Q8K3Y7_RAT      Q8k3y7 rattus norv
 28      172.5 13.1    2     253    2   Q5CAQ0_CHICK    Q5caq0 gallus gall
 29      171   13.0    2     278    2   Q4STX9_TETNG    Q4stx9 tetraodon n
 30      162   12.3    2     239    2   Q5OL61_CHICK    Q5ol61 gallus gall
 31      160   12.1    2     207    2   Q58G74_CHICK    Q58g74 gallus gall
 32      160   12.1    2     279    2   Q7TMV9_MOUSE    Q7tmv9 mus musculu
 33      158   12.0    2      98    2   Q4T6H7_TETNG    Q4t6h7 tetraodon n
 34      157.5 11.9    2     282    1   TNF6_PIG        Q9bea8 sus scrofa
 35      157   11.9    2     261    1   TNFL6_BOVIN     P51749 b tumor nec
 36      157   11.9    1     261    1   TNFL6_MOUSE     P41047 mus musculu
 37      157   11.9    2     279    1   TNFL6_MOUSE     Q54a99 mus musculu
 38      156.5 11.9    2     192    2   Q5VJK8_HUMAN    Q5vjk8 homo sapien
 39      156.5 11.9    2     251    2   Q8NFE9_HUMAN    Q8nfe9 homo sapien
 40      155   11.8    2     280    2   Q86IW5_FELCA    Q86iw5 felis silve
 41      150   11.4    2     261    1   TNFL5_AOTTR     Q9bdn3 c tumor nec
 42      150   11.4    1     261    1   TNFL5_CALJA     Q9bdm3 c tumor nec
 43      149.5 11.3    2     280    1   TNFL5_HUMAN     P29965 h tumor nec
 44      149.5 11.3    1     280    1   TNFL6_MACFA     P63308 m tumor nec
 45      149.5 11.3    1     280    1   TNFL6_MACMU     P63307 m tumor nec
```

ALIGNMENTS

RESULT 1
TNF11_HUMAN

```
ID   TNF11_HUMAN              STANDARD;      PRT;    317 AA.
AC   O14788; O14723; Q96O17; Q9P2Q3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF) [Contains: Tumor necrosis factor ligand
DE   superfamily member 11, membrane form; Tumor necrosis factor ligand
DE   superfamily member 11, soluble form].
GN   Name=TNFSF11; Synonyms=OPGL, RANKL, TRANCE;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow, and Peripheral blood;
RX   MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Lymph node;
RX   MEDLINE=98327661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RA   Ikeda T., Kuroyama H., Hirokawa K.;
RT   "Determination of human RANKL isoforms.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC   TISSUE=Tongue;
RX   MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;
RA   Nagai M., Kyakumoto S., Sato N.;
RT   "Cancer cells responsible for humoral hypercalcemia express mRNA
RT   encoding a secreted form of ODF/TRANCE that induces osteoclast
RT   formation.";
```

RL   Biochem. Biophys. Res. Commun. 269:532-536(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Lung;
RX   MEDLINE=22308257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]

RC   TISSUE=Thymocyte;
RX   MEDLINE=97460112; PubMed=9312122; DOI=10.1074/jbc.272.40.25190;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).

CC   -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC   TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC   Augments the ability of dendritic cells to stimulate naive T-cell
CC   proliferation. May be an important regulator of interactions
CC   between T cells and dendritic cells and may play a role in the
CC   regulation of the T cell-dependent immune response. May also play
CC   an important role in enhanced bone-resorption in humoral
CC   hypercalcemia of malignancy.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
CC   Secreted (isoform 2). A soluble form of isoform 1 arises by
CC   proteolytic processing (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=3;
CC   Name=1;
CC   IsoId=O14788-1; Sequence=Displayed;
CC   Name=2; Synonyms=SODF;
CC   IsoId=O14788-2; Sequence=VSP_006447;
CC   Name=3;
CC   IsoId=O14788-3; Sequence=VSP_006446;
CC   -!- TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
CC   spleen, peripheral blood leukocytes, bone marrow, heart, placenta,
CC   skeletal muscle, stomach and thyroid.
CC   -!- INDUCTION: Up-regulated by T cell receptor stimulation.
CC   -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC   by proteolytic processing (By similarity). The cleavage may be
CC   catalyzed by ADAM17.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.

DR   EMBL; AB061227; BAB71768.1; -; mRNA.
DR   EMBL; AB064270; BAB79695.1; -; mRNA.
DR   EMBL; AB037599; BAA90488.1; -; mRNA.
DR   EMBL; BC074823; AAH74823.1; -; mRNA.
DR   EMBL; BC074890; AAH74890.1; -; mRNA.
DR   EMBL; AF013171; AAC51762.1; -; mRNA.
DR   HSSP; O35235; 1JTZ.
DR   SMR; O14788; 162-317.
DR   Ensembl; ENSG00000120659; Homo sapiens.
DR   HGNC; HGNC:11926; TNFSF11.
DR   MIM; 602642; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   GO; GO:0030316; P:osteoclast differentiation; NAS.
DR   InterPro; IPR006052; TNF family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   SMART; SM00207; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS00049; TNF_2; 1.
KW   Alternative splicing; Cytokine; Developmental protein; Transmembrane.
KW   Differentiation; Glycoprotein; Receptor; Signal-anchor;

FT   CHAIN   1   317   Tumor necrosis factor ligand superfamily
FT   member 11, membrane form.
FT   CHAIN   140   317   Tumor necrosis factor ligand superfamily
FT   member 11, soluble form.
FT   TOPO_DOM   1   47   Cytoplasmic (Potential).
FT   TRANSMEM   48   68   Signal-anchor for type II membrane
FT   protein (Potential).
FT   TOPO_DOM   69   317   Extracellular (Potential).
FT   SITE   139   140   Cleavage (By similarity).
FT   CARBOHYD   171   171   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   198   198   N-linked (GlcNAc...) (Potential).
FT   VARSPLIC   1   73   Missing (in isoform 2).
FT   /FTId=VSP_006447.
FT   VARSPLIC   1   47   Missing (in isoform 3).
FT   /FTId=VSP_006446.
FT   CONFLICT   194   194   A -> G (in Ref. 6).
SQ   SEQUENCE   317 AA; 35478 MW; 76617646348097F CRC64;

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Best Local Similarity   100.0%;
Matches  249;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1  YFRAQMDPNRISEDGTHCIYRILRLRHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQ   60
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Db    69  YFRAQMDPNRISEDGTHCIYRILRLRHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQ  128

Qy    61  KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY  120
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Db   129  KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY  188

Qy   121  HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVTVTKTSIK  180
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Db   189  HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVTVTKTSIK  248

Qy   181  IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   249  IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF  308

Qy   241  GAFKVRDID  249
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Db   309  GAFKVRDID  317
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RESULT 2

ID   Q5T9Y4_HUMAN   PRELIMINARY;   PRT;   317 AA.
Q5T9Y4_HUMAN
AC   Q5T9Y4;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:44:31 ; Search time 42.4525 Seconds
484.925 Million cell updates/sec

Title: US-09-211-297-39_COPY_69_317
Perfect score: 1319
Sequence: 1 YFRAQMDPNRISEDGTHCIY..........LLDPDQDATYFGAFKVRDID 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1319	100.0	317	2	US-08-996-139-13	Sequence 13, Appl
2	1319	100.0	317	2	US-08-995-659-13	Sequence 13, Appl
3	1319	100.0	317	2	US-09-215-649A-13	Sequence 13, Appl
4	1319	100.0	317	2	US-09-052-521C-4	Sequence 4, Appli
5	1319	100.0	317	2	US-09-577-780-13	Sequence 13, Appl
6	1319	100.0	317	2	US-09-577-800-13	Sequence 13, Appl
7	1319	100.0	317	2	US-09-466-496-13	Sequence 13, Appl
8	1319	100.0	317	2	US-09-871-856-13	Sequence 13, Appl
9	1319	100.0	317	2	US-09-871-291-13	Sequence 13, Appl
10	1319	100.0	317	2	US-09-396-937-2	Sequence 2, Appli
11	1319	100.0	317	2	US-09-877-650-13	Sequence 13, Appl
12	1319	100.0	317	2	US-09-865-363-13	Sequence 13, Appl
13	1319	100.0	317	2	US-09-688-459-13	Sequence 13, Appl
14	1319	100.0	317	2	US-09-957-944-6	Sequence 6, Appli
15	1134	86.0	294	2	US-09-995-659A-11	Sequence 11, Appl
16	1134	86.0	294	2	US-08-995-659A-11	Sequence 11, Appl
17	1134	86.0	294	2	US-09-577-780-11	Sequence 11, Appl
18	1134	86.0	294	2	US-09-577-800-11	Sequence 11, Appl
19	1134	86.0	294	2	US-09-466-496-11	Sequence 11, Appl
20	1134	86.0	294	2	US-09-466-496-11	Sequence 11, Appl
21	1134	86.0	294	2	US-09-871-291-11	Sequence 11, Appl
22	1134	86.0	294	2	US-09-871-856-11	Sequence 11, Appl
23	1134	86.0	294	2	US-09-877-650-11	Sequence 11, Appl
24	1134	86.0	294	2	US-09-865-363-11	Sequence 11, Appl
25	1134	86.0	294	2	US-09-688-459-11	Sequence 11, Appl
26	1134	86.0	316	2	US-09-957-944-8	Sequence 8, Appli
27	1127	85.4	316	1	US-08-842-842-7	Sequence 7, Appli
28	1127	85.4	316	2	US-08-989-362-2	Sequence 2, Appli
29	1127	85.4	316	2	US-09-052-521C-2	Sequence 2, Appli
30	1127	85.4	316	2	US-09-671-658A-2	Sequence 2, Appli
31	1127	85.4	316	2	US-09-396-937-4	Sequence 4, Appli
32	1127	85.4	316	2	US-09-396-937-6	Sequence 6, Appli
33	771	58.5	187	2	US-09-396-937-8	Sequence 8, Appli
34	769	58.3	173	2	US-09-396-937-10	Sequence 10, Appl
35	759	57.5	173	2	US-09-396-937-12	Sequence 12, Appl
36	721.5	54.7	188	2	US-09-396-937-14	Sequence 14, Appl
37	711.5	53.9	182	2	US-09-396-937-16	Sequence 16, Appl
38	691	52.4	173	2	US-09-396-937-18	Sequence 18, Appl
39	670	50.8	173	2	US-09-396-937-20	Sequence 20, Appl
40	538	40.8	109	2	US-09-911-777-8	Sequence 8, Appli
41	418	31.7	77	2	US-09-632-287A-11	Sequence 11, Appl
42	418	31.7	77	2	US-09-632-287A-11	Sequence 11, Appl
43	363	27.5	77	2	US-10-286-696-11	Sequence 11, Appl
44	363	27.5	77	2	US-10-286-696-10	Sequence 10, Appl
45	238.5	18.1	291	1	US-08-670-354-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-996-139-13
; Sequence 13, Application US/0899639
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-13

Query Match
Best Local Similarity 100.0%; Score 1319; DB 2; Length 317;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Pred. No. 1.7e-139;
US-08-995-659-13

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Qy    1 YFRAQMDPNRISEDGTHCIYRLRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQ  60
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Qy   61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY  120
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Db  129 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY  188

Qy  121 HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLIATEYLQLMYYVTKTSIK  180
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Db  189 HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLIATEYLQLMYYVTKTSIK  248

Qy  181 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF  240
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Db  249 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF  308

Qy  241 GAFKVRDID  249
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Db  309 GAFKVRDID  317
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RESULT 2
US-08-995-659-13
; Sequence 13, Application US/0899565-9
; Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/813,509
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/064,671
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match
Best Local Similarity 100.0%; Score 1319; DB 2; Length 317;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Pred. No. 1.7e-139;
US-09-215-659-13

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Db  189 HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLIATEYLQLMYYVTKTSIK  248

Qy  181 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF  240
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Qy  241 GAFKVRDID  249
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RESULT 3
US-09-215-649A-13
; Sequence 13, Application US/0921564-9A
; Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
         Galibert, Laurent
         Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: December 21, 2005, 13:02:07 ; Search time 137,154 Seconds
758.559 Million cell updates/sec (without alignments)

Title: US-09-211-297-39_COPY_69_317
Perfect score: 1319
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Scoring table: BLOSUM62
         Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
             Maximum Match 100%
             Listing first 45 summaries

Database :
Published Applications AA_Main:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1319	100.0	249	4	US-10-050-902-221	Sequence 221, App
2	1319	100.0	249	4	US-10-050-898-221	Sequence 221, Appl
3	1319	100.0	249	4	US-10-289-456-82	Sequence 82, Appl
4	1319	100.0	250	4	US-10-338-785A-1	Sequence 1, Appl
5	1319	100.0	250	4	US-10-611-363-1	Sequence 1, Appli
6	1319	100.0	270	4	US-10-289-456-80	Sequence 80, Appl
7	1319	100.0	317	4	US-09-813-329-7	Sequence 7, Appl
8	1319	100.0	317	3	US-09-871-856-13	Sequence 13, Appl
9	1319	100.0	317	6	US-09-957-944-6	Sequence 6, Appl
10	1319	100.0	317	3	US-09-865-363-13	Sequence 13, Appl
11	1319	100.0	317	3	US-09-871-291-13	Sequence 13, Appl
12	1319	100.0	317	3	US-09-877-650-13	Sequence 13, Appl
13	1319	100.0	317	3	US-09-933-915A-2	Sequence 2, Appli
14	1319	100.0	317	3	US-09-151-071-10	Sequence 10, Appl
15	1319	100.0	317	4	US-10-218-547-22	Sequence 22, Appl
16	1319	100.0	317	4	US-10-405-878-13	Sequence 13, Appl
17	1319	100.0	317	4	US-10-167-182-11	Sequence 11, Appl
18	1319	100.0	317	4	US-10-310-793-28	Sequence 28, Appl
19	1319	100.0	317	4	US-10-460-623-11	Sequence 11, Appl
20	1319	100.0	317	4	US-10-289-456-79	Sequence 79, Appl
21	1319	100.0	317	4	US-10-202-062-22	Sequence 22, Appl
22	1319	100.0	317	4	US-10-664-801-2	Sequence 2, Appl
23	1319	100.0	317	4	US-10-381-160-6	Sequence 6, Appli
24	1319	100.0	317	4	US-10-799-345-12	Sequence 12, Appli
25	1319	100.0	317	5	US-10-399-116-6	Sequence 6, Appli
26	1319	100.0	317	5	US-10-802-133-13	Sequence 13, Appli
27	1319	100.0	317	5	US-10-825-898-4	Sequence 4, Appli
28	1319	100.0	317	5	US-10-854-300-11	Sequence 11, Appl
29	1319	100.0	317	5	US-10-129-595-1	Sequence 1, Appli
30	1319	100.0	317	5	US-10-451-200-6	Sequence 6, Appli
31	1319	100.0	317	5	US-10-999-523-8	Sequence 8, Appli
32	1319	100.0	317	6	US-11-028-780-22	Sequence 22, Appli
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35	1319	100.0	317	6	US-11-142-736-7	Sequence 7, Appl
36	1301	98.6	246	4	US-10-167-182-17	Sequence 17, Appl
37	1301	98.6	246	4	US-10-440-623-17	Sequence 17, Appl
38	1301	98.6	246	4	US-10-854-300-17	Sequence 17, Appl
39	1301	98.6	245	4	US-11-135-521-17	Sequence 17, Appl
40	1293	98.0	245	4	US-09-873-829-2	Sequence 2, Appli
41	1293	98.0	245	3	US-09-933-915A-10	Sequence 10, Appl
42	1292	98.0	244	3	US-10-017-910-2	Sequence 2, Appli
43	1292	98.0	244	4	US-09-210-951-42	Sequence 42, Appli
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45	1292	98.0	244	4	US-10-050-898-222	Sequence 222, App

ALIGNMENTS

RESULT 1
US-10-050-902-221

Sequence 221, Application US/10050902
Publication No. US2003017S290A1
GENERAL INFORMATION:
APPLICANT: Renner, Wolfgang A.
APPLICANT: Bachmann, Martin
APPLICANT: Tissot, Alain
APPLICANT: Maurer, Patrick
APPLICANT: Lechner, Franziska
APPLICANT: Sebbel, Peter
APPLICANT: Piossek, Christine
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0190004
CURRENT APPLICATION NUMBER: US/10/050,902
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,379
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/288,549
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/326,998
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
SOFTWARE: Patentin Ver. 2.1
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 221
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-10-050-902-221

Query Match   100.0%;   Score 1319;   DB 4;   Length 249;
Best Local Similarity   100.0%;
Matches   249;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Db    1 YFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQ 60

Qy   61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY 120
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Db   61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY 120

Qy  121 HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIK 180
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Qy  181 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF 240
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Db    181 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF 240

Qy    241 GAFKVRDID 249
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RESULT 2
US-10-050-898-221

; Sequence 221, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Frey, Peter
; APPLICANT: Staufenbiel, Matthias
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 221
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-898-221

Query Match   100.0%; Score 1319; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.3e-122;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY 120
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Qy  181 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF 240
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Qy  241 GAFKVRDID 249
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RESULT 3
US-10-289-456-82

; Sequence 82, Application US/10289456
; Publication No. US20040032112A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-289-456-82

Query Match   100.0%; Score 1319; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.3e-122;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  121 HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMYVVTKTSIK 180
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Qy  181 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF 240
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Qy  241 GAFKVRDID 249
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RESULT 4
US-10-338-785A-1

; Sequence 1, Application US/10338785A
; Publication No. US20030219864A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hubert, Rene S.
; APPLICANT: El Yazal, Jamal
; TITLE OF INVENTION: No. US20030219864A1e1 Variants of RANKL Protein
; FILE REFERENCE: A-71486
; CURRENT APPLICATION NUMBER: US/10/338,785A
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank Acc. No. US20030219864A1 AAB86811
; DATABASE ENTRY DATE: 1997-11-21

OM protein - protein search, using sw model

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

Run on: December 21, 2005, 13:03:52 ; Search time 7.75574 Seconds
228.978 Million cell updates/sec
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Title: US-09-211-297-39_COPY_69_317
Perfect score: 1319
Sequence: 1 YFRAQMDPNRISEDGTHCIY..........LLDPDQDATYFGAFKVRDID 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   Published_Applications_AA_New:*
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8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	AA ID	Description
1	538	40.8	109	7	US-11-065-669-8	Sequence 8, Appli
2	236.5	17.9	281	6	US-11-821-234-1288	Sequence 1288, Ap
3	235.5	17.9	266	7	US-10-082-544-10	Sequence 10, Appli
4	232.5	17.6	281	7	US-11-077-272-2	Sequence 2, Appli
5	232.5	17.6	391	7	US-11-105-172-4	Sequence 4, Appli
6	147.5	11.2	359	7	US-11-105-172-2	Sequence 2, Appli
7	134	10.2	240	6	US-10-987-663-6	Sequence 6, Appli
8	133	10.1	157	7	US-11-010-954-1	Sequence 1, Appli
9	133	10.1	157	7	US-11-053-750-1	Sequence 1, Appli
10	133	10.1	157	7	US-11-053-749-1	Sequence 1, Appli
11	133	10.1	157	7	US-11-108-001-12	Sequence 12, Appli
12	133	10.1	158	7	US-11-082-544-4	Sequence 4, Appli
13	133	10.1	164	7	US-11-108-001-2	Sequence 2, Appli
14	133	10.1	180	7	US-11-082-544-8	Sequence 8, Appli
15	92.5	7.0	177	6	US-10-999-866-61	Sequence 61, Appl
16	92.5	7.0	205	6	US-10-995-561-1028	Sequence 1028, Ap
17	92.5	7.0	205	6	US-10-995-561-1029	Sequence 1029, Ap
18	86.5	6.6	104	7	US-11-065-669-5	Sequence 5, Appli
19	85	6.4	220	7	US-11-054-515-3233	Sequence 3233, Ap
20	77.5	5.9	290	6	US-11-054-198-2	Sequence 2, Appli
21	77	5.8	290	7	US-10-524-198-2	Sequence 2, Appli
22	76.5	5.8	219	7	US-11-054-515-3237	Sequence 3237, Appli
23	76.5	5.8	243	7	US-11-054-515-3236	Sequence 3236, Ap
24	74.5	5.6	239	7	US-11-054-515-3232	Sequence 3232, Ap
25	74.5	5.6	943	6	US-10-475-204-34	Sequence 34, Appl
26	73.5	5.6	207	7	US-11-054-515-3234	Sequence 3234, Ap
27	73	5.5	188	7	US-11-054-515-3235	Sequence 3235, Ap
28	73	5.5	536	6	US-10-131-826A-490	Sequence 490, App
29	72	5.5	389	7	US-11-088-686-1	Sequence 1, Appli
30	72	5.5	389	7	US-11-088-686-3	Sequence 3, Appli
31	72	5.5	389	7	US-11-088-686-5	Sequence 5, Appli
32	72	5.5	389	7	US-10-878-556A-42	Sequence 42, Appli
33	72	5.5	389	7	US-11-088-686-9	Sequence 9, Appli
34	72	5.5	389	7	US-11-088-686-7	Sequence 7, Appli
35	72	5.5	389	7	US-11-088-686-11	Sequence 11, Appli
36	72	5.5	1001	6	US-11-088-686-13	Sequence 13, Appl
37	71.5	5.4	1151	7	US-10-467-962B-81	Sequence 81, Appli
38	71.5	5.4	1151	7	US-11-128-420-10	Sequence 10, Appl
39	71	5.4	1467	6	US-10-507-956-1	Sequence 1, Appli
40	70.5	5.3	369	7	US-11-112-882-4	Sequence 4, Appli
41	70.5	5.3	369	7	US-11-055-822-32	Sequence 32, Appli
42	70	5.3	585	6	US-10-742-634-3	Sequence 3, Appli
43	70	5.3	152	7	US-10-742-634-17	Sequence 17, Appli
44	70	5.3	178	7	US-11-054-515-3229	Sequence 3229, Ap
45	70	5.3	285	6	US-10-131-826A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-11-065-669-8

; Sequence 8, Application US/11065669
; Publication No. US20050244411A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Kalled, Susan
; TITLE OF INVENTION: BAFF, INHIBITORS THEREOF AND THEIR USE IN THE
; TITLE OF INVENTION: MODULATION OF B-CELL RESPONSE
; FILE REFERENCE: 08201.0024-04000
; CURRENT APPLICATION NUMBER: US/11/065,669
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 10/045,574
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-065-669-8

Query Match 40.8%; Score 538; DB 7; Length 109;
Best Local Similarity 75.5%; Pred. No. 1.4e-46;
Matches 108; Conservative 0; Mismatches 1; Indels 34; Gaps 2;

Qy   93 EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANI 152
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||YANI
Db   1 EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWGKISNM------------------YANI 43

Qy 153 CFRHHETSGDLATEYLQLMVYVVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGF 212
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44 CFRHHETSGDLATEYLQLMVVVTKTSIKIP-----------------SEFHFYSINVGGF 86

Qy 213 FKLRSGEEISIEVSNPSLLDPDQ 235
         ||||||||||||||||||||||
Db   87 FKLRSGEEISIEVSNPSLLDPDQ 109

RESULT 2

US-10-821-234-1288
Sequence 1288, Application US/10821234
; Publication No. US2005255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1288
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1288

Query Match   17.9%;   Score 236.5; DB 6; Length 281;
Best Local Similarity   25.1%; Pred. No. 3.1e-16;
Matches   67; Conservative 53; Mismatches 102; Indels 45; Gaps 10;

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Qy      1 YFRAQMD--PNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGA 58
            |:   :   ::::                              :  :  :
Db     37 YFTNELKQMQDKYSKSGIACF-----LKED-----DSYWDPNDEESMNSPCWQVKW----- 82

Qy     59 VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF----------AHLT-----IN 103
Db     83 ---QLRQLVRKMILRTSEETI-----STVQEKQQNISPLVRERGPQRVAAHITGTRGRSN 134

Qy    104 ATDIPSGSHKVSL-----SSWYHDR-GWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHE 158
Db    135 TLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQE 194

Qy    159 TSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSSTKYWSGNSEFHFYSINVGGFFKLRSG 218
Db    195 EIKENTKNDKQMYQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKEN 253

Qy    219 EEISIEVSNPSLLDPDQDATYFGAFKV 245
Db    254 DRIFVSVTNEHLIDMDHEASFGAFLV 280
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RESULT 3
US-11-082-544-10
Sequence 10, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
; APPLICANT: King, I.
; APPLICANT: Clairmont, C.
; APPLICANT: Lin, S.
; APPLICANT: Belcourt, M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;   TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
; FILE REFERENCE: 8002-059
; CURRENT APPLICATION NUMBER: US/11/082,544
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/09/645,415
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/157,581
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/157,637
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion construct
US-11-082-544-10

Query Match   17.9%;   Score 235.5; DB 7; Length 266;
Best Local Similarity   25.3%; Pred. No. 3.6e-16;
Matches   65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;

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Qy      9 NRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVG 68
           ::::                              :  :  :            |: |
Db      1 DKYSKSGIACF-----LKED-----DSYWDPNDEESMNSPCWQVKW--------QLRQLVR 74

Qy     69 SQHIRAEKAMVDGSWLDLAKRSKLEAQPF----------AHLT------INATDIPSGSHK 113
Db     75 KMILRTSEETI-----STVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNE 129

Qy    114 VSL-----SSWYHDR-GWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYL 168
Db    130 KALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDK 189

Qy    169 QLMVYVTKTSIKIPSSHTLMKGGSSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNP 228
Db    190 QMYQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNE 248

Qy    229 SLLDPDQDATYFGAFKV 245
Db    249 HLIDMDHEASFGAFLV 265
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RESULT 4
US-11-077-272-2
Sequence 2, Application US/11077272
; Publication No. US20050244927A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, WOON-LAM SUSAN
; APPLICANT: SWARTZ, JAMES R.
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDES
; FILE REFERENCE: P2019R1
; CURRENT APPLICATION NUMBER: US/11/077,272
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/552,678
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-272-2

Query Match   17.6%;   Score 232.5; DB 7; Length 281;
Best Local Similarity   25.1%; Pred. No. 7.6e-16;
Matches   67; Conservative 52; Mismatches 103; Indels 45; Gaps 10;

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Db     37 YFTNELKQMQDKYSKSGIACF-----LKED-----DSYWDPNDEESMNSPCWQVKW----- 82

Qy     59 VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF----------AHLT-----IN 103
Db     83 ---QLRQLVRKMILRTSEETI-----STVQEKQQNISPLVRERGPQRVAAHITGTRGRSN 134

Qy    104 ATDIPSGSHKVSL-----SSWYHDR-GWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHE 158
Db    135 TLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHGKGFYYIYSQTYFRFQE 194

Qy    159 TSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSSTKYWSGNSEFHFYSINVGGFFKLRSG 218
Db    195 EIKENTKNDKQMYQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKEN 253

Qy    219 EEISIEVSNPSLLDPDQDATYFGAFKV 245
Db    254 DRIFVSVTNEHLIDMDHEASFGAFLV 280
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:44:31 ; Search time 2.89836 Seconds

484.925 Million cell updates/sec

Title: 84
Perfect score: 84
Sequence: 1 VYVVKTSIKIPSSHNLM 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	84	100.0	17	2	US-09-052-521C-35	Sequence 35, Appl
2	84	100.0	173	2	US-09-396-937-10	Sequence 10, Appl
3	84	100.0	173	2	US-09-396-937-12	Sequence 12, Appl
4	84	100.0	173	2	US-09-396-937-18	Sequence 18, Appl
5	84	100.0	187	2	US-09-396-937-8	Sequence 8, Appl
6	84	100.0	188	2	US-09-396-937-14	Sequence 14, Appl
7	84	100.0	294	2	US-08-996-139-11	Sequence 11, Appl
8	84	100.0	294	2	US-08-995-659-11	Sequence 11, Appl
9	84	100.0	294	2	US-09-215-649A-11	Sequence 11, Appl
10	84	100.0	294	2	US-09-577-780-11	Sequence 11, Appl
11	84	100.0	294	2	US-09-577-800-11	Sequence 11, Appl
12	84	100.0	294	2	US-09-466-496-11	Sequence 11, Appl
13	84	100.0	294	2	US-09-871-856-11	Sequence 11, Appl
14	84	100.0	294	2	US-09-871-291-11	Sequence 11, Appl
15	84	100.0	294	2	US-09-877-650-11	Sequence 11, Appl
16	84	100.0	294	2	US-09-865-363-11	Sequence 11, Appl
17	84	100.0	294	2	US-09-688-459-11	Sequence 11, Appli
18	84	100.0	316	1	US-08-842-842-7	Sequence 7, Appli
19	84	100.0	316	2	US-08-989-362-2	Sequence 2, Appli
20	84	100.0	316	2	US-09-052-521C-2	Sequence 2, Appli
21	84	100.0	316	2	US-09-671-658A-2	Sequence 2, Appli
22	84	100.0	316	2	US-09-396-937-4	Sequence 4, Appli
23	84	100.0	316	2	US-09-396-937-6	Sequence 6, Appli
24	84	100.0	316	2	US-09-957-944-8	Sequence 8, Appli
25	74	88.1	317	2	US-08-996-139-13	Sequence 13, Appl
26	74	88.1	317	2	US-08-995-659-13	Sequence 13, Appl
27	74	88.1	317	2	US-09-215-649A-13	Sequence 13, Appl
28	74	88.1	317	2	US-09-052-521C-4	Sequence 4, Appli
29	74	88.1	317	2	US-09-577-780-13	Sequence 13, Appl
30	74	88.1	317	2	US-09-577-800-13	Sequence 13, Appl
31	74	88.1	317	2	US-09-466-496-13	Sequence 13, Appl
32	74	88.1	317	2	US-09-871-856-13	Sequence 13, Appl
33	74	88.1	317	2	US-09-871-291-13	Sequence 13, Appl
34	74	88.1	317	2	US-09-396-937-2	Sequence 2, Appl
35	74	88.1	317	2	US-09-396-937-16	Sequence 16, Appl
36	74	88.1	317	2	US-09-957-944-6	Sequence 6, Appl
37	74	88.1	317	2	US-09-688-459-13	Sequence 13, Appl
38	74	88.1	317	2	US-09-865-363-13	Sequence 13, Appl
39	71	84.5	182	2	US-09-396-937-20	Sequence 20, Appl
40	69	82.1	173	2	US-09-628-665-4	Sequence 4, Appli
41	54	64.3	12	2	US-09-628-665-23	Sequence 23, Appl
42	54	64.3	16	2	US-09-628-665-8	Sequence 8, Appli
43	54	63.1	109	2	US-09-911-777-8	Sequence 8, Appli
44	50	59.5	10	2	US-09-628-665-6	Sequence 6, Appli
45	50	59.5	11	2	US-09-628-665-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-052-521C-35

Sequence 35, Application US/09052521C

Patent No. 6316608

GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-052-521C-35

Query Match   100.0%; Score 84; DB 2; Length 17;
Best Local Similarity   100.0%; Pred. No. 1.7e-07;
Matches   17; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VYVVKTSIKIPSSHNLM 17
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Db   1 VYVVKTSIKIPSSHNLM 17

RESULT 2
US-09-396-937-10

Sequence 10, Application US/09396937

Patent No. 6645500

GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: HALKIER, Torben
APPLICANT: HAANING, Jesper
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
FILE REFERENCE: 22021 PC 1
CURRENT APPLICATION NUMBER: US/09/396,937
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10

; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNA encoding
; OTHER INFORMATION: murine OPGL, residues 158-316, fused to His tag
US-09-396-937-10

Qy   1 VYVVKTSIKIPSSHNLM 17
              |||||||||||||||||
Db   96 VYVVKTSIKIPSSHNLM 112

Query Match   100.0%; Score 84; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches   17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-09-396-937-12
; Sequence 12, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion of
; OTHER INFORMATION: murine OPGL, residues 158-316 with C to S
; OTHER INFORMATION: mutation, and His tag
US-09-396-937-12

Qy   1 VYVVKTSIKIPSSHNLM 17
              |||||||||||||||||
Db   96 VYVVKTSIKIPSSHNLM 112

Query Match   100.0%; Score 84; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches   17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-396-937-18
; Sequence 18, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion between
; OTHER INFORMATION: murine OPGL, residues 158-316 with tetanus toxoid

; OTHER INFORMATION: P2 epitope introduced, and His tag
US-09-396-937-18

Qy   1 VYVVKTSIKIPSSHNLM 17
              |||||||||||||||||
Db   96 VYVVKTSIKIPSSHNLM 112

Query Match   100.0%; Score 84; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches   17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-09-396-937-8
; Sequence 8, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR
; OTHER INFORMATION: product with optimum codons for E. coli and P.
; OTHER INFORMATION: pastoris expression
US-09-396-937-8

Qy   1 VYVVKTSIKIPSSHNLM 17
              |||||||||||||||||
Db   110 VYVVKTSIKIPSSHNLM 126

Query Match   100.0%; Score 84; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches   17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
US-09-396-937-14
; Sequence 14, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion of
; OTHER INFORMATION: murine OPGL, residues 158-316 modified by
; OTHER INFORMATION: introduction of tetanus toxoid P30 epitope, and
; OTHER INFORMATION: His tag
US-09-396-937-14

Query Match   100.0%; Score 84; DB 2; Length 188;

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 13:02:07 ; Search time 9.36393 seconds
             (without alignments)
             758.559 Million cell updates/sec

Title: US-09-211-297-34
Perfect score: 84
Sequence: 1 VYVVKTSIKIPSSHNLM 17

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 10%
                 Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
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             4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	84	100.0	17	5	US-10-825-898-35	Sequence 35, Appl
2	84	100.0	18	3	US-10-825-898-36	Sequence 36, Appl
3	84	100.0	160	3	US-09-779-050A-14	Sequence 14, Appl
4	84	100.0	170	3	US-09-791-153A-76	Sequence 76, Appl
5	84	100.0	170	4	US-10-289-456-99	Sequence 99, Appl
6	84	100.0	173	4	US-10-664-801-10	Sequence 10, Appl
7	84	100.0	173	4	US-10-664-801-12	Sequence 12, Appl
8	84	100.0	187	4	US-10-664-801-18	Sequence 18, Appl
9	84	100.0	187	4	US-10-664-801-8	Sequence 8, Appli
10	84	100.0	188	4	US-10-664-801-14	Sequence 14, Appl
11	84	100.0	193	4	US-10-289-456-96	Sequence 96, Appl
12	84	100.0	199	4	US-10-050-902-224	Sequence 224, App
13	84	100.0	199	4	US-10-050-898-224	Sequence 224, App
14	84	100.0	199	4	US-10-289-456-86	Sequence 86, Appl
15	84	100.0	244	4	US-10-167-182-16	Sequence 16, Appl
16	84	100.0	244	4	US-10-460-623-16	Sequence 16, Appl
17	84	100.0	244	5	US-10-854-300-16	Sequence 16, Appl
18	84	100.0	244	5	US-11-135-521-16	Sequence 16, Appl
19	84	100.0	247	4	US-10-050-902-223	Sequence 223, App
20	84	100.0	247	4	US-10-050-898-223	Sequence 223, Appl
21	84	100.0	247	4	US-10-289-456-85	Sequence 85, Appl
22	84	100.0	249	4	US-10-338-785A-3	Sequence 3, Appli
23	84	100.0	249	4	US-10-611-363-3	Sequence 3, Appli
24	84	100.0	294	3	US-09-871-856-11	Sequence 11, Appl
25	84	100.0	294	3	US-09-865-363-11	Sequence 11, Appl
26	84	100.0	294	3	US-09-871-291-11	Sequence 11, Appl
27	84	100.0	294	3	US-09-877-650-11	Sequence 11, Appl
28	84	100.0	294	4	US-10-405-878-11	Sequence 11, Appl
29	84	100.0	294	5	US-10-802-133-11	Sequence 11, Appl
30	84	100.0	316	3	US-09-957-944-8	Sequence 8, Appli
31	84	100.0	316	3	US-09-079-569-7	Sequence 7, Appli
32	84	100.0	316	3	US-09-873-829-4	Sequence 4, Appli
33	84	100.0	316	3	US-09-933-915A-16	Sequence 16, Appli
34	84	100.0	316	4	US-09-873-910-4	Sequence 4, Appli
35	84	100.0	316	4	US-10-017-910-4	Sequence 4, Appli
36	84	100.0	316	4	US-10-105-057-2	Sequence 2, Appli
37	84	100.0	316	4	US-10-272-411-19	Sequence 19, Appl
38	84	100.0	316	4	US-10-326-052-2	Sequence 2, Appli
39	84	100.0	316	4	US-10-272-328A-19	Sequence 19, Appli
40	84	100.0	316	4	US-10-167-182-1	Sequence 1, Appl
41	84	100.0	316	4	US-10-460-623-1	Sequence 1, Appli
42	84	100.0	316	4	US-10-664-801-6	Sequence 6, Appli
43	84	100.0	316	4	US-10-799-345-10	Sequence 10, Appli
44	84	100.0	316	5	US-10-825-898-2	Sequence 2, Appli
45	84	100.0	316	5	US-10-854-300-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-825-898-35

; Sequence 35, Application US/10825898
; Publication No. US2005000340OA1
US-10-825-898-35

GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS
FILE REFERENCE: A-451K REV 09-10-03 54SEQ
CURRENT APPLICATION NUMBER: US/10/825,898
CURRENT FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: US/10/825,898
PRIOR FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: US 09/052,521
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: US 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: US 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.1

SEQ ID NO 35
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide

Query Match   100.0%; Score 84; DB 5; Length 17;
Best Local Similarity   100.0%; Pred. No. 1.5e-07;
Matches   17; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VYVVKTSIKIPSSHNLM 17
          |||||||||||||||||
Db   1 VYVVKTSIKIPSSHNLM 17

RESULT 2
US-10-825-898-36

; Sequence 36, Application US/10825898
; Publication No. US2005000340OA1
US-10-825-898-36

GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS
FILE REFERENCE: A-451K REV 09-10-03 54SEQ
CURRENT APPLICATION NUMBER: US/10/825,898
CURRENT FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: US/10/825,898
PRIOR FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: US 09/052,521

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;  PRIOR FILING DATE: 1998-03-30
;  PRIOR APPLICATION NUMBER: US 08/880,855
;  PRIOR FILING DATE: 1997-06-23
;  PRIOR APPLICATION NUMBER: US 08/842,842
;  PRIOR FILING DATE: 1997-04-16
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: Patentin version 3.1
;  SEQ ID NO 36
;  LENGTH: 18
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Synthetic Oligonucleotide
US-10-825-898-36

Query Match            100.0%;  Score 84;  DB 5;  Length 18;
Best Local Similarity  100.0%;  Pred. No. 1.6e-07;
Matches   17;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1 VYVVKTSIKIPSSHNLM 17
       |||||||||||||||||
Db   1 VYVVKTSIKIPSSHNLM 17
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RESULT 3
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US-09-779-050A-14
Sequence 14, Application US/0977905050A
Patent No. US2002016041641
GENERAL INFORMATION:
   APPLICANT: BOYLE, WILLIAM
   APPLICANT: HSU, HAILING
   TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
   FILE REFERENCE: A-570B
   CURRENT APPLICATION NUMBER: US/09/779,050A
   CURRENT FILING DATE: 2001-02-12
   PRIOR APPLICATION NUMBER: 60/181,800
   PRIOR FILING DATE: 2000-02-11
   NUMBER OF SEQ ID NOS: 52
   SOFTWARE: Patentin version 3.0
;  SEQ ID NO 14
;  LENGTH: 160
;  TYPE: PRT
;  ORGANISM: Mus musculus
US-09-779-050A-14

Query Match            100.0%;  Score 84;  DB 3;  Length 160;
Best Local Similarity  100.0%;  Pred. No. 1.8e-06;
Matches   17;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1 VYVVKTSIKIPSSHNLM 17
       |||||||||||||||||
Db  83 VYVVKTSIKIPSSHNLM 99
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RESULT 4
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US-09-791-153A-76
Sequence 76, Application US/0979115353A
Publication No. US20030103978A1
GENERAL INFORMATION:
   APPLICANT: Deshpande, Rajendra
   APPLICANT: Hitz, Anna
   APPLICANT: Boyle, William
   APPLICANT: Sullivan, John
   TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
   FILE REFERENCE: A-633A
   CURRENT APPLICATION NUMBER: US/09/791,153A
   CURRENT FILING DATE: 2001-07-17
   PRIOR APPLICATION NUMBER: 09/511,139
   PRIOR FILING DATE: 2000-02-23
   NUMBER OF SEQ ID NOS: 154
   SOFTWARE: Patentin version 3.0
;  SEQ ID NO 76
;  LENGTH: 170
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RESULT 5
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US-10-289-456-99
Sequence 99, Application US/10289456
Publication No. US20040033211A1
GENERAL INFORMATION:
   APPLICANT: Bachmann, Martin
   APPLICANT: Maurer, Patrick
   APPLICANT: Spohn, Gunther
   TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
   FILE REFERENCE: 1700.0330001
   CURRENT APPLICATION NUMBER: US/10/289,456
   CURRENT FILING DATE: 2002-11-07
   PRIOR APPLICATION NUMBER: PCT/IB02/00166
   PRIOR FILING DATE: 2002-01-21
   PRIOR APPLICATION NUMBER: US 10/050,902
   PRIOR FILING DATE: 2002-01-18
   PRIOR APPLICATION NUMBER: US 60/396,635
   PRIOR FILING DATE: 2002-07-19
   PRIOR APPLICATION NUMBER: US 60/331,045
   PRIOR FILING DATE: 2001-11-07
   NUMBER OF SEQ ID NOS: 170
   SOFTWARE: Patentin version 3.2
;  SEQ ID NO 99
;  LENGTH: 170
;  TYPE: PRT
;  ORGANISM: Mus sp.
US-10-289-456-99

Query Match            100.0%;  Score 84;  DB 4;  Length 170;
Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
Matches   17;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1 VYVVKTSIKIPSSHNLM 17
       |||||||||||||||||
Db  84 VYVVKTSIKIPSSHNLM 100
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;  TYPE: PRT
;  ORGANISM: Mus musculus
US-09-791-153A-76

Query Match            100.0%;  Score 84;  DB 3;  Length 170;
Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
Matches   17;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1 VYVVKTSIKIPSSHNLM 17
       |||||||||||||||||
Db  93 VYVVKTSIKIPSSHNLM 109
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RESULT 6
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US-10-664-801-10
Sequence 10, Application US/10664801
Publication No. US20040115199A1
GENERAL INFORMATION:
   APPLICANT: M&E Biotech A/S
   APPLICANT: HALKIER, Torben
   APPLICANT: HAANING, Jesper
   TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
   FILE REFERENCE: 22021 PC 1
   CURRENT APPLICATION NUMBER: US/10/664,801
   CURRENT FILING DATE: 2003-09-17
   PRIOR APPLICATION NUMBER: US/09/396,937
   PRIOR FILING DATE: 1999-09-15
   NUMBER OF SEQ ID NOS: 35
   SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 10
;  LENGTH: 173
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: DNA encoding
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 13:03:52 ; Search time 0.529508 Seconds
                                    (without alignments)
                                    228.978 Million cell updates/sec

Title: US-09-211-297-34
Perfect score: 84
Sequence: 1 VYVVKTSIKIPSSHNLM 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Databases :   Published Applications_AA_New:*
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                2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	63.1	109	7	US-11-065-669-8	Sequence 8, Appli
2	44.0	717	6	US-10-793-626-3022	Sequence 3022, Ap
3	41.7	269	6	US-11-077-550-68	Sequence 68, Appl
4	35	113	6	US-10-821-234-1684	Sequence 1684, Ap
5	34	351	6	US-10-793-626-3282	Sequence 3282, Ap
6	34	374	6	US-10-467-657-5088	Sequence 5088, Ap
7	33.5	39	6	US-11-060-023-10	Sequence 10, Appl
8	33	2174	6	US-10-467-657-2174	Sequence 2174, Ap
9	33	96	6	US-10-467-657-8984	Sequence 8984, Ap
10	33	155	7	US-11-069-642-97	Sequence 97, Appl
11	33	198	7	US-11-069-642-25	Sequence 25, Appl
12	33	208	6	US-10-980-388-81	Sequence 81, Appl
13	33	238	7	US-11-069-642-127	Sequence 127, Appli
14	33	431	7	US-11-069-642-1	Sequence 1, Appl
15	33	437	7	US-11-069-642-92	Sequence 92, Appl
16	33	438	7	US-11-069-642-49	Sequence 49, Appl
17	33	438	7	US-11-069-642-51	Sequence 51, Appl
18	33	438	7	US-11-069-642-53	Sequence 53, Appl
19	33	438	7	US-11-069-642-55	Sequence 55, Appl
20	33	438	7	US-11-069-642-57	Sequence 57, Appl
21	33	438	7	US-11-069-642-59	Sequence 59, Appl
22	33	438	7	US-11-069-642-61	Sequence 61, Appl
23	33	438	7	US-11-069-642-63	Sequence 63, Appl
24	33	490	7	US-11-131-826A-310	Sequence 310, Appl
25	33	619	6	US-10-763-712A-35	Sequence 35, Appl
26	33	734	7	US-11-093-274-40	Sequence 40, Appl
27	33	949	7	US-11-077-550-68	Sequence 68, Appl
28	33	1420	7	US-11-077-550-110	Sequence 110, App
29	32	64	7	US-10-467-657-7122	Sequence 7122, Ap
30	32	101	7	US-11-053-076-51	Sequence 51, Appl
31	32	111	7	US-11-053-076-163	Sequence 163, App
32	32	215	6	US-10-793-626-596	Sequence 596, App
33	32	215	6	US-10-793-626-2258	Sequence 2258, Ap
34	32	257	6	US-10-467-962B-73	Sequence 73, Appl
35	32	317	6	US-10-689-742-166	Sequence 166, App
36	32	356	7	US-11-055-822-972	Sequence 972, App
37	32	356	7	US-11-055-822-1052	Sequence 1052, Ap
38	32	437	7	US-11-055-822-970	Sequence 970, App
39	32	437	7	US-11-082-389-180	Sequence 180, App
40	32	477	7	US-11-055-822-1050	Sequence 1050, App
41	32	478	6	US-11-055-822-768	Sequence 768, App
42	32	567	6	US-10-793-626-768	Sequence 768, App
43	32	1234	6	US-10-131-826A-476	Sequence 476, Ap
44	32	2725	6	US-10-467-657-4224	Sequence 4224, App
45	31	102	7	US-11-053-076-162	Sequence 162, App

ALIGNMENTS

RESULT 1
US-11-065-669-8
; Sequence 8, Application US/11065669
; Publication No. US20050244411A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Kalled, Susan
; TITLE OF INVENTION: BAFF, INHIBITORS THEREOF AND THEIR USE IN THE
; TITLE OF INVENTION: MODULATION OF B-CELL RESPONSE
; FILE REFERENCE: 08201.0024-04000
; CURRENT APPLICATION NUMBER: US/11/065,669
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 10/045,574
; PRIOR FILING DATE: 2005-11-07
; PRIOR APPLICATION NUMBER: 09/911,777
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 2001-07-24
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/143,228
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-065-669-8

Query Match   63.1%;   Score 53; DB 7; Length 109;
Best Local Similarity   91.7%;   Pred. No. 0.0067;
Matches   11; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 VYVVKTSIKIPS 12
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Db   63 VYVTKTSIKIPS 74

RESULT 2
US-10-793-626-3022
; Sequence 3022, Application US/10793626
; Publication No. US20050254578A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626

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;   CURRENT FILING DATE: 2004-03-04
;   PRIOR APPLICATION NUMBER: 60/164,258
;   PRIOR FILING DATE: 1999-11-09
;   NUMBER OF SEQ ID NOS: 4472
;   SOFTWARE: Patentin Ver. 2.1
;
;   SEQ ID NO 3022
;   LENGTH: 717
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3022

Query Match             44.0%;  Score 37;  DB 6;  Length 717;
Best Local Similarity   46.2%;  Pred. No. 39;
Matches    6;  Conservative   4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YVVKTSIKIPSSH 14
              |:||  ||| ||:||
Db        198 YIVKQGVKILNNH 210


RESULT 3
US-10-821-234-1684
Sequence 1684, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
;   APPLICANT: Labat, Ivan
;   APPLICANT: Stache-Crain, Birgit
;   APPLICANT: Andarmani, Susan
;   APPLICANT: Tang, Y. Tom
;   TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;   FILE REFERENCE: 821A
;   CURRENT APPLICATION NUMBER: US/10/821,234
;   CURRENT FILING DATE: 2004-04-07
;   PRIOR APPLICATION NUMBER: US 60/462,047
;   PRIOR FILING DATE: 2003-04-07
;   NUMBER OF SEQ ID NOS: 1704
;   SOFTWARE: pt_SEQ_genes Version 1.0
;   SEQ ID NO 1684
;   LENGTH: 269
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-821-234-1684

Query Match             41.7%;  Score 35;  DB 6;  Length 269;
Best Local Similarity   50.0%;  Pred. No. 28;
Matches    6;  Conservative   3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 TSIKIPSSHNLM 17
              |:|| |  ||| ||::
Db        186 TDIKIATGHNII 197


RESULT 4
US-10-793-626-3282
Sequence 3282, Application US/10793626
Publication No. US20050254478A1
GENERAL INFORMATION:
;   APPLICANT: KIMMERLY, WILLIAM JOHN
;   TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;   FILE REFERENCE: PU34800S
;   CURRENT APPLICATION NUMBER: US/10/793,626
;   CURRENT FILING DATE: 2004-03-04
;   PRIOR APPLICATION NUMBER: 60/164,258
;   PRIOR FILING DATE: 1999-11-09
;   NUMBER OF SEQ ID NOS: 4472
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 3282
;   LENGTH: 113
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-10-793-626-3282

Query Match             40.5%;  Score 34;  DB 6;  Length 113;
Best Local Similarity   42.9%;  Pred. No. 16;
Matches    6;  Conservative   4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 YVVVKTSIKIPSSH 14
              | :|  |:|::|
Db         56 VSVASTLMKLPNTH 69


RESULT 5
US-10-467-657-5088
Sequence 5088, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
;   APPLICANT: CHIRON SpA
;   APPLICANT: FONTANA Maria Rita
;   APPLICANT: PIZZA Mariagrazia
;   APPLICANT: MASIGNANI Vega
;   APPLICANT: MONACI Elisabetta
;   TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;   FILE REFERENCE:
;   CURRENT APPLICATION NUMBER: US/10/467,657
;   CURRENT FILING DATE: 2003-08-11
;   PRIOR APPLICATION NUMBER: GB-0103424.8
;   PRIOR FILING DATE: 2001-02-12
;   NUMBER OF SEQ ID NOS: 9218
;   SOFTWARE: SeqWin99, version 1.04
;   SEQ ID NO 5088
;   LENGTH: 351
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5088

Query Match             40.5%;  Score 34;  DB 6;  Length 351;
Best Local Similarity   40.0%;  Pred. No. 58;
Matches    6;  Conservative   4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 YVVKTSIKIPSSHNL 16
              :|| :  ||  |||
Db        275 HIINPNNKRPISHNL 289


RESULT 6
US-11-060-023-10
Sequence 10, Application US/11060023
Publication No. US20050255531A1
GENERAL INFORMATION:
;   APPLICANT: Aventis Pharma Deutschland GmbH
;   TITLE OF INVENTION: Process for identifying modulators of G protein coupled
;   TITLE OF INVENTION: receptors
;   FILE REFERENCE: AVE D-2000/A033 englisch
;   CURRENT APPLICATION NUMBER: US/11/060,023
;   CURRENT FILING DATE: 2005-02-17
;   PRIOR APPLICATION NUMBER: US/09/899,295
;   PRIOR FILING DATE: 2003-07-06
;   NUMBER OF SEQ ID NOS: 17
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 10
;   LENGTH: 374
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-060-023-10

Query Match             39.9%;  Score 33.5;  DB 7;  Length 374;
Best Local Similarity   47.1%;  Pred. No. 76;
Matches    8;  Conservative   4;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          1 VYVVKTSI--KIPSSH 14
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 21, 2005, 12:34:10 ; Search time 11.5656 Seconds
                                       (without alignments)
                                       645.834 Million cell updates/sec

Title: US-09-211-297-34
Perfect Score: 84
Sequence: 1 VYVVKTSIKIPSSHNLM 17

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : A_Geneseq_21:*
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  2: geneseqp1990s:*
  3: geneseqp2000s:*
  4: geneseqp2001s:*
  5: geneseqp2002s:*
  6: geneseqp2003as:*
  7: geneseqp2003bs:*
  8: geneseqp2004s:*
  9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	84	100.0	17	2	Aaw83198	Aaw83198 Murine os
2	84	100.0	18	2	Aaw83199	Aaw83199 Murine os
3	84	100.0	139	3	Aay91023	Aay91023 Mouse OBM
4	84	100.0	155	6	Abr39854	Abr39854 RANK liga
5	84	100.0	155	7	Adc03334	Adc03334 Murine re
6	84	100.0	155	7	Adi53055	Adi53055 Human RAN
7	84	100.0	160	3	Aab08272	Aab08272 Amino aci
8	84	100.0	170	4	Aau08386	Aau08386 Mouse PLA
9	84	100.0	170	3	Adj82132	Adj82132 Protein f
10	84	100.0	173	3	Aay84422	Aay84422 A murine
11	84	100.0	173	3	Aay84425	Aay84425 DNA encod
12	84	100.0	173	3	Aay84421	Aay84421 Amino aci
13	84	100.0	187	3	Aay84420	Aay84420 Amino aci
14	84	100.0	188	3	Aay84423	Aay84423 An osteop
15	84	100.0	193	7	Adj82129	Adj82129 Protein f
16	84	100.0	199	5	Abg94285	Abg94285 Mouse RAN
17	84	100.0	199	5	Abg80597	Abg80597 Mouse rec
18	84	100.0	199	7	Adj82119	Adj82119 Protein f
19	84	100.0	216	7	Adb16999	Adb16999 Murine RA
20	84	100.0	244	2	Aaw83019	Aaw83019 A murine
21	84	100.0	247	5	Abg94284	Abg94284 Mouse RAN
22	84	100.0	247	5	Abg80596	Abg80596 Mouse rec
23	84	100.0	247	7	Adj82118	Adj82118 Protein f
24	84	100.0	249	6	Ada50081	Ada50081 Mouse wil
25	84	100.0	294	2	Aaw69956	Aaw69956 NF-kB rec
26	84	100.0	294	2	Aaw68292	Aaw68292 NF-kB rec
27	84	100.0	294	2	Aae08737	Aae08737 Murine re
28	84	100.0	294	2	Aae04425	Aae04425 Murine re
29	84	100.0	294	4	Aae01992	Aae01992 Murine RA
30	84	100.0	294	5	Aae26102	Aae26102 Mouse RAN
31	84	100.0	294	7	Adb16986	Adb16986 Murine re
32	84	100.0	294	7	Adc73000	Adc73000 Murine RA
33	84	100.0	294	7	Adc78266	Adc78266 Murine RA
34	84	100.0	294	7	Adg46721	Adg46721 Murine RA
35	84	100.0	294	9	Adw09027	Adw09027 Murine re
36	84	100.0	316	2	Aaw83017	Aaw83017 Osteoclas
37	84	100.0	316	2	Aaw83194	Aaw83194 Human ost
38	84	100.0	316	2	Aaw59654	Aaw59654 Amino aci
39	84	100.0	316	2	Aay17874	Aay17874 Murine TR
40	84	100.0	316	3	Aay91024	Aay91024 Mouse OBM
41	84	100.0	316	3	Aay84418	Aay84418 Amino aci
42	84	100.0	316	3	Aay84419	Aay84419 Amino aci
43	84	100.0	316	4	Aau78289	Aau78289 Mouse TRA
44	84	100.0	316	5	Adr29338	Adr29338 Mouse RAN
45	84	100.0	316	6	Abr42071	Abr42071 Human RAN

ALIGNMENTS

RESULT 1
AAW83198
ID   AAW83198 standard; peptide; 17 AA.
XX
AC   AAW83198;
XX
DT   11-FEB-1999 (first entry)
XX
DE   Murine osteoprotegerin binding protein EF loop peptide.
XX
KW   Osteoprotegerin binding protein; OPG binding protein; arthritis;
KW   osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW   hypercalcaemia; osteoclast differentiation and activation receptor;
KW   Paget's disease.
XX
OS   Mus sp.
XX
PN   WO9846751-A1.
XX
PD   22-OCT-1998.
XX
PF   15-APR-1998; 98WO-US007584.
XX
PR   16-APR-1997; 97US-00842842.
PR   23-JUN-1997; 97US-00880855.
PR   30-MAR-1998; 98US-00052521.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ;
XX
PT   WPI; 1998-594578/50.
XX
DR   WPI; 1998-594578/50.
XX
PS   Example 11; Page 55; 47pp; English.
XX
CC   The present sequence represents peptide from murine osteoprotegerin (OPG)
CC   binding protein. Host cells transfected with vectors containing nucleic
CC   acid molecules encoding OPG binding protein are used to produce
CC   recombinant OPG binding protein. OPG binding protein is used in binding
CC   assays to determine osteoprotegerin (OG) in biological samples; to screen
CC   for specific binding agents (particularly agonists and antagonists,
CC   including intracellular proteins); to raise Ab (useful in immunoassays
CC   for detection of OPG binding protein) and to identify compounds that

Nucleic acid encoding osteoprotegerin binding protein - useful for, e.g.
treating bone diseases by modulating osteoclast differentiation and for
diagnosis.

```
CC   modulate binding of OPG binding protein to osteoclast differentiation and
CC   activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC   binding protein can be used to detect OPG binding protein-encoding
CC   sequences, e.g. screening for related sequences, also to produce
CC   transgenic animal models while complementary sequences are used for
CC   antisense regulation of OPG binding protein expression. Modulators of OPG
CC   binding protein, particularly soluble forms of OPG binding protein or Ab,
CC   are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss
CC   caused by arthritis or metastases, hypercalcaemia, Paget's disease,
CC   periodontal disease, osteoporosis, loosening of prostheses, optionally in
CC   combination with agents that promote bone growth
XX
SQ   Sequence 17 AA;

Qy
Db

Query Match             100.0%;   Score 84;   DB 2;   Length 17;
Best Local Similarity   100.0%;   Pred. No. 1.4e-07;
Matches  17;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy    1 VYVVKTSIKIPSSHNLM 17
        |||||||||||||||||
Db    1 VYVVKTSIKIPSSHNLM 17


RESULT 2
AAW83199
ID   AAW83199 standard; peptide; 18 AA.
XX
AC   AAW83199;
XX
DT   11-FEB-1999  (first entry)
XX
DE   Murine osteoprotegerin binding protein EF loop-Cys peptide.
XX
KW   Osteoprotegerin binding protein; OPG binding protein; arthritis;
KW   osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW   hypercalcaemia; osteoclast differentiation and activation receptor;
KW   Paget's disease.
XX
OS   Mus sp.
XX
XX
PN   WO9846751-A1.
XX
PD   22-OCT-1998.
XX
PF   15-APR-1998;    98WO-US007584.
XX
PR   16-APR-1997;    97US-00842842.
PR   23-JUN-1997;    97US-00880855.
PR   30-MAR-1998;    98US-00052521.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ;
XX
DR   WPI; 1998-594578/50.
XX
PT   Nucleic acid encoding osteoprotegerin binding protein - useful for, e.g.
PT   treating bone diseases by modulating osteoclast differentiation and for
PT   diagnosis.
XX
PS   Example 11; Page 55; 47pp; English.
XX
CC   The present sequence represents peptide from murine osteoprotegerin (OPG)
CC   binding protein. Host cell transfected with vectors containing nucleic
CC   acid molecules encoding OPG binding protein are used to produce
CC   recombinant OPG binding protein. OPG binding protein is used in binding
CC   assays to determine osteoprotegerin (OG) in biological samples; to screen
CC   for specific binding agents (particularly agonists and antagonists,
CC   including intracellular proteins); to raise Ab (useful in immunoassays
CC   for detection of OPG binding protein) and to identify compounds that
CC   modulate activation of OPG binding protein to osteoclast differentiation and
CC   activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC  `binding protein can be used to detect OPG binding protein-encoding
```

```
CC   sequences, e.g. screening for related sequences, also to produce
CC   transgenic animal models while complementary sequences are used for
CC   antisense regulation of OPG binding protein expression. Modulators of OPG
CC   binding protein, particularly soluble forms of OPG binding protein or Ab,
CC   are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss
CC   caused by arthritis or metastases, hypercalcaemia, Paget's disease,
CC   periodontal disease, osteoporosis, loosening of prostheses, optionally in
CC   combination with agents that promote bone growth
XX
SQ   Sequence 18 AA;

Query Match             100.0%;   Score 84;   DB 2;   Length 18;
Best Local Similarity   100.0%;   Pred. No. 1.4e-07;
Matches  17;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy    1 VYVVKTSIKIPSSHNLM 17
        |||||||||||||||||
Db    1 VYVVKTSIKIPSSHNLM 17


RESULT 3
AAY91023
ID   AAY91023 standard; protein; 139 AA.
XX
AC   AAY91023;
XX
DT   05-SEP-2000  (first entry)
XX
DE   Mouse OBM protein sequence SEQ ID NO:8.
XX
KW   Mouse; osteoclastogenesis inhibitory factor binding molecule; OCIF; OBM;
KW   osteoclast; bone absorption promoting factor; vitamin D3; PTH;
KW   parathyroid hormone.
XX
OS   Mus sp.
XX
PN   JP200010239O-A.
XX
PD   11-APR-2000.
XX
PF   30-SEP-1998;    98JP-00292971.
XX
PR   30-SEP-1998;    98JP-00292971.
XX
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
PA   (YSNE-) YS NEW TECHNOLOGY KENKYUSHO.
XX
DR   WPI; 2000-332087/29.
DR   N-PSDB; AAA39155.
XX
PT   A DNA and preparation of a protein by using it.
XX
PS   Example 2; Page 14; 18pp; Japanese.
XX
CC   The present invention describes a genomic DNA encoding a protein having
CC   an activity of supporting or promoting differentiation and maturation of
CC   osteoclasts. The genomic DNA encoding a protein has the following
CC   properties: (a) combines specifically with osteoclastogenesis inhibitory
CC   factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw)
CC   of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide
CC   gel electrophoresis) under a nonreductive condition and the apparent mw
CC   when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c) has
CC   an activity of supporting or promoting differentiation and maturation of
CC   osteoclast in the co-culture of mouse osteoblast-like stroma cell and
CC   mouse spleen cell in the presence of a bone absorption promoting factor
CC   such as active type vitamin D3 and parathyroid hormone (PTH). The protein
CC   can be used as a drug and a research reagent. The present sequence
CC   represents a mouse OCIF binding molecule (OBM) from the present invention
XX
SQ   Sequence 139 AA;

Query Match             100.0%;   Score 84;   DB 3;   Length 139;
Best Local Similarity   100.0%;   Pred. No. 1.5e-06;
```

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:47:51 ; Search time 1.92295 seconds

OM protein - protein search, using sw model
(without alignments)
850.612 Million cell updates/sec

Title: US-09-211-297-34
Perfect Score: 84
Sequence: 1 VYVVKTSIKIPSSHNLM 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	45	53.6	206	2	G86279	F14I17.27 protein
2	44.5	53.0	311	2	B70441	ribose-phosphate d
3	43	51.2	232	1	I83349	CS6 subunits chape
4	43	51.2	377	2	S67448	hypothetical prote
5	41	48.8	612	2	AI3493	oligopeptide-bindi
6	40	47.6	115	2	F81358	probable periplasm
7	40	47.6	311	2	C23701	olfactory receptor
8	40	47.6	1235	2	T17457	SARA protein - Afr
9	39.5	47.0	917	2	T05430	hypothetical prote
10	39	46.4	176	2	C86824	hypothetical prote
11	39	46.4	262	2	T49066	hypothetical prote
12	39	46.4	288	2	B98278	hypothetical prote
13	39	46.4	288	2	AI3005	conserved hypothet
14	39	46.4	334	2	A70101	hypothetical prote
15	39	46.4	360	2	T15639	hypothetical prote
16	39	46.4	603	2	T40528	palmitoyl-protein
17	39	46.4	659	2	F72568	probable acylamino
18	39	46.4	799	2	B71478	probable cell divi
19	39	46.4	1109	2	B90127	DNA-directed RNA p
20	39	46.4	1227	2	T48028	hypothetical prote
21	39	46.4	1802	2	S69703	HKR1 protein precu
22	38.5	45.8	409	2	A46297	beta-1,6-N-acetylg
23	38.5	45.8	699	2	T16109	hypothetical prote
24	38	45.2	135	2	PN0530	G protein-coupled
25	38	45.2	294	2	B69445	conserved hypothet
26	38	45.2	332	2	H84129	sugar ABC transpor
27	38	45.2	510	1	S15620	L1 protein - human
28	38	45.2	672	2	E90294	hypothetical prote
29	38	45.2	899	2	G71453	hypothetical prote
30	38	45.2	1038	2	S52522	hypothetical prote
31	38	45.2	1517	2	T38912	hypothetical integ
32	37.5	44.6	119	2	AH3459	hypothetical prote
33	37	44.0	72	2	AA2528	hypothetical prote
34	37	44.0	76	2	AH2120	hypothetical prote
35	37	44.0	174	2	F97114	uncharacterized co
36	37	44.0	291	2	S28299	hypothetical prote
37	37	44.0	307	2	T34143	hypothetical prote
38	37	44.0	327	2	G83921	hypothetical prote
39	37	44.0	334	2	E75153	glyceraldehyde 3-p
40	37	44.0	370	2	S52699	hypothetical prote
41	37	44.0	377	2	AB0087	probable flagellar
42	37	44.0	433	2	AD1164	H-transporting AT
43	37	44.0	433	2	AD1523	H-transporting AT
44	37	44.0	452	2	JC6561	UDP-N-acetylmuramo
45	37	44.0	506	1	ACRYG1	nicotinic acetylch

ALIGNMENTS

RESULT 1
G86279
F14I17.27 protein - Arabidopsis thaliana
G86279
F14I17.27 protein - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86279
R;Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86279
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <STO>
A;Cross-references: UNIPROT:Q9M9R4; UNIPARC:UPI00000A0A22; GB:AE005172; NID:g7262692; PI
C;Genetics:
A;Map position: 1

Qy   1 VYVVKTSIKIPSSHNL 16
            ||||| || ||||||
Db   142 VYFVATSFKNPSYHRL 157

Query Match	53.6%;	Score 45;	DB 2;	Length 206;	
Best Local Similarity	62.5%;	Pred. No. 2.5;			
Matches 10;	Conservative	0;	Mismatches	6;	Indels 0; Gaps 0;

RESULT 2
B70441
ribose-phosphate diphosphokinase (EC 2.7.6.1) - Aquifex aeolicus
B70441
ribose-phosphate diphosphokinase (EC 2.7.6.1) - Aquifex aeolicus
N;Alternate names: phosphoribosylpyrophosphate synthetase
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: B70441
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: B70441
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-311 <AQF>
A;Cross-references: UNIPROT:O67556; UNIPARC:UPI00005668B; GB:AE00748; NID:g2983960; PI
A;Experimental source: strain VF5

C;Genetics:
A;Gene: prs
C;Function:
A;Pathway: nucleotide biosynthesis
C;Superfamily: ribose-phosphate pyrophosphokinase catalytic chain
C;Pathway: diphosphotransferase; magnesium; nucleotide biosynthesis
F;215-227//Region: phosphoribosylpyrophosphate binding
C;Keywords: diphosphotransferase; magnesium; nucleotide biosynthesis

```
Query Match        53.0%;  Score 44.5;  DB 2;  Length 311;
Best Local Similarity 58.8%;  Pred. No. 4.7;
Matches  10;  Conservative  3;  Mismatches  3;  Indels  1;  Gaps  1;

Qy    1 VVVKTSIKIPSSHNLM 17
          ||| |||||| | ||||
Db   53 VTVI-TSLSNPVNHNLM 68
```

RESULT 3
I83349
CS6 subunits chaperone - Escherichia coli
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I83349
R;Willshaw, G.A.; Smith, H.R.; McConnell, M.M.; Rowe, B.
FEMS Microbiol. Lett. 49, 473-478, 1988
A;Title: Cloning of genes encoding coli-surface (CS) antigens in enterotoxigenic Escheri
A;Reference number: 160266
A;Accession: I83349
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-232 <RES>
A;Cross-references: UNIPROT:P53518; UNIPARC:UPI0000001284F5; EMBL:U04844; NID:g442375; PID
C;Superfamily: chaperone protein papD
C;Keywords: molecular chaperone

```
Query Match        51.2%;  Score 43;  DB 1;  Length 232;
Best Local Similarity 41.2%;  Pred. No. 6.3;
Matches  7;  Conservative  5;  Mismatches  5;  Indels  0;  Gaps  0;

Qy    1 VVVKTSIKIPSSHNLM 17
          :||:||||:|:|||| |
Db   83 IKIKTNIKLPDSQESM 99
```

RESULT 4
S67448
hypothetical protein YOR322c homolog SPAC1F12.05 - fission yeast (Schizosaccharomyces po
C;Species: Schizosaccharomyces pombe
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S67448; T38063
R;McLean, J.; Harris, D.
submitted to the EMBL Data Library, March 1996
A;Reference number: S67448
A;Accession: S67448
A;Molecule type: DNA
A;Residues: 1-377 <MCL>
A;Cross-references: UNIPROT:Q10347; UNIPARC:UPI000013A8E4; EMBL:Z69944; NID:g1217974; PI
R;McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, March 1996
A;Reference number: 221766
A;Accession: T38063
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-377 <MC2>
A;Cross-references: UNIPARC:UPI000013A8E4; EMBL:Z69944; PIDN:CAA93809.1; GSPDB:GN000066;
C;Experimental source: strain 972h-; cosmid c1F12
C;Genetics:
A;Gene: SPAC1F12.05

```
Query Match        51.2%;  Score 43;  DB 2;  Length 377;
Best Local Similarity 63.6%;  Pred. No. 11;
Matches  7;  Conservative  3;  Mismatches  1;  Indels  0;  Gaps  0;
```
A;Map position: 1

```
Qy    2 YVVKTSIKIPS 12
          | ||| :|||||
Db  131 YILKTRVKIPS 141
```

RESULT 5
AI3493
oligopeptide-binding protein appA precursor [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AI3493
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi
A;Cross-references: UNIPROT:Q8YEE3; UNIPARC:UPI000005B272; GB:AE008917; PIDN:AAL53116.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1935
A;Accession: AI3493
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-612 <KUR>
A;Reference number: AD3252; PMID:11756688
C;Superfamily: periplasmic oligopeptide-binding protein
A;Map position: I

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Query Match        48.8%;  Score 41;  DB 2;  Length 612;
Best Local Similarity 80.0%;  Pred. No. 41;
Matches  8;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy    7 SIKIPSSHNL 16
          ||||||:|||
Db  524 SAKIPGSHNL 533
```

RESULT 6
F81358
probable periplasmic protein Cj0854c [imported] - Campylobacter jejuni (strain NCTC 1116
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: F81358
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: F81358
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-115 <PAR>
A;Cross-references: UNIPROT:Q9PP69; UNIPARC:UPI000000C1D64; GB:AL139076; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj0854c
C;Superfamily: Helicobacter pylori hypothetical protein jhp0221

```
Query Match        47.6%;  Score 40;  DB 2;  Length 115;
Best Local Similarity 53.8%;  Pred. No. 10;
Matches  7;  Conservative  3;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    4 VKTSIKIPSSHNL 16
          :|||||||||| ||
Db   59 IKTAYKVPSIQNL 71
```

RESULT 7
C23701
olfactory receptor F6 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: C23701

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:35:06 ; Search time 11.7049 Seconds
(without alignments)
1024.696 Million cell updates/sec

Title: US-09-211-297-34
Perfect score: 84
Sequence: 1 VYVVKTSIKIPSSHNLM 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	84	100.0	316	1	TNF11_MOUSE	O35235	m tumor nec
2	84	100.0	318	1	TNF11_RAT	Q9ee2	r tumor nec
3	74	88.1	244	2	Q54A98_HUMAN	Q54a98	homo sapien
4	74	88.1	317	2	TNF11_HUMAN	O14788	h tumor nec
5	74	88.1	317	2	Q5T9Y4_HUMAN	Q5t9y4	homo sapien
6	47	56.0	378	2	Q5L899_BACFN	Q5l899	bacteroides
7	47	56.0	378	2	Q64NJ9_BACFR	Q64nj9	bacteroides
8	45	53.6	206	2	Q9M9R4_ARATH	Q9m9r4	arabidopsis
9	45	53.6	312	2	Q8VG32_MOUSE	Q8vg32	mus musculu
10	45	53.6	315	2	Q7TRH2_MOUSE	Q7trh2	mus musculu
11	45	53.6	315	2	Q8VFU3_MOUSE	Q8vfu3	mus musculu
12	45	53.6	315	2	Q8VFU4_MOUSE	Q8vfu4	mus musculu
13	45	53.6	320	2	Q8VF26_MOUSE	Q8vf26	mus musculu
14	44.5	53.0	311	1	KPRS_AQUAE	O67556	aquifex aeo
15	44	52.4	311	2	Q8VGC2_MOUSE	Q8vgc2	mus musculu
16	44	52.4	406	2	Q9LKA2_ARATH	Q9lka2	arabidopsis
17	44	52.4	420	2	Q8LPR5_ARATH	Q8lpr5	arabidopsis
18	44	52.4	504	2	ACHE_XENLA	P49580	xenopus lae
19	44	52.4	727	2	Q9W7F9_CHICK	Q9w7f9	gallus gall
20	43	51.2	192	2	Q6VZE6_CNPV	Q6vze6	canarypox v
21	43	51.2	232	2	CSSC1_ECOLI	P53518	escherichia
22	43	51.2	350	2	Q923H4_MOUSE	Q923h4	mus musculu
23	43	51.2	377	1	YDAS_SCHPO	O10347	schizosacch
24	42	50.0	125	1	ATG8_PICPA	O8nJj4	pichia past
25	42	50.0	176	2	Q9K571_LACLC	Q9k571	lactococcus
26	42	50.0	205	2	Q8NA88_HUMAN	Q8na88	homo sapien
27	42	50.0	217	2	Q6QA70_HUMAN	Q6qa70	homo sapien
28	42	50.0	225	2	Q8NGU1_HUMAN	Q8ngu1	homo sapien
29	42	50.0	288	2	Q6W061_MOUSE	Q6w061	mus musculu
30	42	50.0	310	2	Q8VFD8_MOUSE	Q8vfd8	mus musculu
31	42	50.0	312	2	Q8VFH8_MOUSE	Q8vfh8	mus musculu
32	42	50.0	314	1	OR9A4_HUMAN	Q8ngu2	homo sapien
33	42	50.0	314	2	Q6IFI4_HUMAN	Q6ifi4	homo sapien
34	42	50.0	336	2	Q6FQE8_CANGA	Q6fqe8	candida gla
35	42	50.0	485	2	Q59WH5_CANAL	Q59wh5	candida alb
36	42	50.0	505	2	Q6S3H5_CHON	Q6s3h5	hypnos mono
37	42	50.0	530	2	Q8IJ67_PLAF7	Q8ij67	plasmodium
38	42	50.0	778	1	DACT1_MOUSE	Q8r4a3	mus musculu
39	42	50.0	836	2	DACT1_HUMAN	Q9nyf0	homo sapien
40	42	50.0	877	2	Q5CTV9_CRYPV	Q5ctv9	cryptospori
41	42	50.0	897	2	Q5CMPO_CRYHO	Q5cmpo	cryptospori
42	42	50.0	992	1	ANR18_HUMAN	Q8ivf6	homo sapien
43	42	50.0	992	2	Q5SY86_HUMAN	Q5sy86	homo sapien
44	42	50.0	1072	2	Q4WRN9_ASPFU	Q4wrn9	aspergillus
45	42	50.0	1776	2	Q7R2L9_GIALA	Q7r2l9	giardia lam

ALIGNMENTS

RESULT 1
TNF11_MOUSE

ID   TNF11_MOUSE   STANDARD;   PRT;   316 AA.
AC   O35235; O35306; Q9JJK8; Q9JJK9; Q9R1Y0;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF) [Contains: Tumor necrosis factor ligand
DE   superfamily member 11, membrane form; Tumor necrosis factor ligand
DE   superfamily member 11, soluble form].
GN   Name=Tnfsf11; Synonyms=Opgl, Rankl, Trance;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Hybridoma;
RX   MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RP   TISSUE=Thymic lymphoma;
RX   MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow;
RX   MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [4]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow stroma;

RX   MEDLINE=98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
RA   Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
RA   Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
RA   Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT   "Osteoclast differentiation factor is a ligand for
RT   osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RT   to TRANCE/RANKL.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN   [5]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   STRAIN=129;
RX   MEDINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
RA   Ueda M., Higashio K., Yasuda H., Shima N., Murakami A.,
RA   Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RT   "Cloning and characterization of the gene encoding mouse osteoclast
RT   differentiation factor.";
RL   Gene 230:121-127(1999).
RN   [6]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1, 2 AND 3).
RX   MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
RA   Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT   "Determination of three isoforms of the receptor activator of nuclear
RT   factor-kappaB ligand and their differential expression in bone and
RT   thymus.";
RL   Endocrinology 142:1419-1426(2001).
RN   [7]
RP   PROTEIN SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
RX   MEDLINE=99240759; PubMed=10244132; DOI=10.1074/jbc.274.19.13613;
RA   Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
RA   Schlondorff J., Tempst P., Choi Y., Biobel C.P.;
RT   "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
RT   converting enzyme-like protease in shedding of TRANCE, a TNF family
RT   member involved in osteoclastogenesis and dendritic cell survival.";
RL   J. Biol. Chem. 274:13613-13618(1999).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
RX   MEDLINE=21464816; PubMed=11581298;
RA   Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
RT   "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
RT   of receptor-ligand specificity.";
RL   J. Clin. Invest. 108:971-979(2001).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
RX   MEDLINE=21839021; PubMed=11734492; DOI=10.1074/jbc.M10652520O;
RA   Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
RT   "Crystal structure of the extracellular domain of mouse RANK ligand at
RT   2.2-A resolution.";
RL   J. Biol. Chem. 277:6631-6636(2002).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC   TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC   Augments the ability of dendritic cells to stimulate naive T-cell
CC   proliferation. May be an important regulator of interactions
CC   between T cells and dendritic cells and may play a role in the
CC   regulation of the T cell-dependent immune response. May also play
CC   an important role in enhanced bone-resorption in humoral
CC   hypercalcemia of malignancy.
CC   -!- SUBUNIT: Homotrimer.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC   (isoforms 1 and 2); Cytoplasmic (isoform 3).
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=3;
CC   Name=1;
CC   IsoId=O35235-1; Sequence=Displayed;
CC   Name=2;
CC   IsoId=O35235-2; Sequence=VSP_006449;
CC   Name=3;
CC   IsoId=O35235-3; Sequence=VSP_006448;
CC   -!- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
CC   but not in nonlymphoid tissues and is abundantly expressed in T
CC   cells but not in B cells. A high level expression is also seen in
CC   the trabecular bone and lung.
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC   by proteolytic processing. The cleavage may be catalyzed by
CC   ADAM17. A further shorter soluble form was observed.
CC   -!- DISEASE: Deficiency in Tnfsf11 results in failure to form lobulo-
CC   alveolar mammary structures during pregnancy, resulting in death
CC   of newborns. Trance-deficient mice show severe osteopetrosis, with
CC   no osteoclasts, marrow spaces, or tooth eruption, and exhibit
CC   profound growth retardation at several skeletal sites, including
CC   the limbs, skull, and vertebrae and have marked chondrodysplasia,
CC   with thick, irregular growth plates and a relative increase in
CC   hypertrophic chondrocytes.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AF013170; AAC71061.1; -; mRNA.
DR   EMBL; AF019048; AAB86812.1; -; mRNA.
DR   EMBL; AF053713; AAC40113.1; -; mRNA.
DR   EMBL; AB008426; BAA25425.1; -; mRNA.
DR   EMBL; AB022039; BAA36970.1; -; Genomic_DNA.
DR   EMBL; AB032771; BAA97257.1; -; mRNA.
DR   EMBL; AB032772; BAA97258.1; -; mRNA.
DR   EMBL; AB032772; BAA97259.1; -; mRNA.
DR   EMBL; AB036798; BAA97259.1; -; mRNA.
DR   PDB; 1IQA; X-ray; A/B/C=157-316.
DR   PDB; 1JTZ; X-ray; X/Y/Z=156-316.
DR   Ensembl; ENSMUSG00000022015; Mus musculus.
DR   MGI; MGI:1100089; Tnfsf11.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0045453; P:bone resorption; IDA.
DR   GO; GO:0007515; P:lymph gland development; IDA.
DR   GO; GO:0009887; P:organogenesis; IMP.
DR   GO; GO:0001503; P:ossification; IMP.
DR   GO; GO:0045672; P:positive regulation of osteoclast different...; IDA.
DR   GO; GO:0051260; P:protein homooligomerization; IDA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1; FALSE_NEG.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   3D-structure; Alternative splicing; Cytokine; Developmental protein;
KW   Differentiation; Direct protein sequencing; Glycoprotein; Receptor;
KW   Signal-anchor; Transmembrane.
FT   CHAIN   1   316   Tumor necrosis factor ligand superfamily
FT   member 11, membrane form.
FT   CHAIN   139   316   Tumor necrosis factor ligand superfamily
FT   member 11, soluble form.
FT   TOPO_DOM   1   48   Cytoplasmic (Potential).
FT   TRANSMEM   49   69   Signal-anchor for type II membrane
FT   protein (Potential).
FT   TOPO_DOM   70   316   Extracellular (Potential).
FT   SITE   138   139   Cleavage.
FT   CARBOHYD   197   197   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   262   262   N-linked (GlcNAc...) (Potential).
FT   VARSPLIC   1   1   Missing (in isoform 3).
FT   /FTId=VSP_006448.
FT   VARSPLIC   14   44   SSEMGSSGPGVPHEGPLHPAPSAPAPPPA -> TP (in
FT   isoform 2).
FT   /FTId=VSP_006449.
FT   CONFLICT   99   99   G -> D (in Ref. 2).
FT   CONFLICT   141   143   Missing (in Ref. 5).
FT   STRAND   164   169
FT   TURN   171   172
FT   STRAND   181   182
FT   STRAND   186   187
FT   TURN   191   192
FT   STRAND   194   196
FT   STRAND   198   201

```
                GenCore version 5.1.6
                Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:          December 21, 2005, 12:35:06 ; Search time 18.5902 Seconds
                 (without alignments)
                 1024.696 Million cell updates/sec

Title:           148
Perfect score:   148
Sequence:        1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:   2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       UniProt_05.80:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	148	100.0	316	1	TNF11_MOUSE	O35235 m tumor nec
2	140	94.6	318	1	TNF11_RAT	Q9ese2 r tumor nec
3	136	91.9	244	1	Q54A98_HUMAN	Q54a98 homo sapien
4	136	91.9	317	1	TNF11_HUMAN	O14788 h tumor nec
5	136	91.9	317	2	Q5T9Y4_HUMAN	Q5t9y4 homo sapien
6	88	59.5	117	2	Q5XLH0_RABIT	Q5xlh0 oryctolagus
7	76	51.4	95	2	Q6UWL7_HUMAN	Q6uwl7 homo sapien
8	76	51.4	95	2	Q6UY13_HUMAN	Q6uy13 homo sapien
9	61.5	41.6	157	2	Q9C4K2_9EURY	Q9c4k2 uncultured
10	59	39.9	456	1	MNTH_BRUME	P65544 brucella me
11	59	39.9	456	1	MNTH_BRUSU	P65545 brucella su
12	59	39.9	456	1	Q57C68_BRUAB	Q57c68 brucella ab
13	59	39.9	157	2	Q9C4G1_9EURY	Q9c4g1 uncultured
14	58.5	39.5	157	2	Q9C4H5_9EURY	Q9c4h5 uncultured
15	58.5	39.5	157	2	Q9C4H7_9EURY	Q9c4h7 uncultured
16	58.5	39.5	157	2	Q9C4I3_9EURY	Q9c4i3 uncultured
17	58.5	39.5	157	2	Q9C4J1_9EURY	Q9c4j1 uncultured
18	58.5	39.5	163	2	Q7ZAE6_9EURY	Q7zae6 uncultured
19	58	39.2	371	2	Q8QOC2_METMA	Q8qoc2 methanosarc
20	57	38.5	255	2	Q41VP8_AZOVI	Q41vp8 azotobacter
21	56.5	38.2	157	2	Q9C4G6_9EURY	Q9c4g6 uncultured
22	56.5	38.2	157	2	Q9C4I8_9EURY	Q9c4i8 uncultured
23	56.5	38.2	162	2	Q6SEI7_9EURY	Q6sei7 uncultured
24	56.5	38.2	211	2	Q75NC5_9ARCH	Q75nc5 uncultured
25	56.5	38.2	224	2	Q6VVF0_9ARCH	Q6vvf0 uncultured
26	56.5	38.2	235	2	Q6VVF2_9ARCH	Q6vvf2 uncultured
27	56.5	38.2	235	2	Q6VVF3_9ARCH	Q6vvf3 uncultured
28	56.5	38.2	235	2	Q6VVF5_9ARCH	Q6vvf5 uncultured
29	56.5	38.2	253	2	Q5EGK0_9EURY	Q5egk0 uncultured
30	56.5	38.2	235	2	Q5EGK6_9EURY	Q5egk6 uncultured
31	56.5	38.2	254	2	Q5EGK5_9EURY	Q5egk5 uncultured
32	56.5	38.2	254	2	Q5EGJ9_9EURY	Q5egj9 uncultured
33	56.5	38.2	254	2	Q64C70_9ARCH	Q64c70 uncultured
34	56.5	38.2	561	2	Q7NRU9_CHRVO	Q7nru9 chromobacte
35	56	37.8	334	2	Q4IZG3_AZOVI	Q4izg3 azotobacter
36	56	37.8	756	2	Q6JI92_9EURY	Q6ji92 uncultured
37	55.5	37.5	162	2	Q6VVE9_9ARCH	Q6vve9 uncultured
38	55.5	37.5	224	2	Q6VVE9_9ARCH	Q6vve9 uncultured
39	55.5	37.5	254	2	Q5EGJ8_9EURY	Q5egj8 uncultured
40	55.5	37.5	254	2	Q5EGJ6_9EURY	Q5egj6 uncultured
41	55.5	37.5	561	2	Q648Y3_9ARCH	Q648y3 uncultured
42	55	37.2	606	2	Q6VUA1_9ARCH	Q6vua1 uncultured
43	54.5	36.8	561	2	Q4TR89_9SPHN	Q4tr89 erythrobact
44	54.5	36.8	156	2	Q6ZXA8_9EURY	Q6zxa8 uncultured
45	54.5	36.8	157	2	Q9C4H0_9EURY	Q9c4h0 uncultured

ALIGNMENTS

RESULT 1
TNF11_MOUSE

```
ID   TNF11_MOUSE   STANDARD;   PRT;   316 AA.
AC   O35235; O35306; Q9JJK8; Q9JJK9; Q9R1Y0;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF) [Contains: Tumor necrosis factor ligand
DE   superfamily member 11, membrane form; Tumor necrosis factor ligand
DE   superfamily member 11, soluble form].
GN   Name=Tnfsf11; Synonyms=Opgl, Rankl, Trance;
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Hybridoma;
RX   MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).
RN   [2]
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RC   TISSUE=Thymic lymphoma;
RX   MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow;
RX   MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [4]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow stroma;
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RX   MEDLINE=98184848; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
RA   Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
RA   Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
RA   Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT   "Osteoclast differentiation factor is a ligand for
RT   osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RT   to TRANCE/RANKL.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN   [5]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   STRAIN=129;
RX   MEDLINE=9921075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
RA   Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA   Ueda M., Higashio K.;
RT   "Cloning and characterization of the gene encoding mouse osteoclast
RT   differentiation factor.";
RL   Gene 230:121-127(1999).
RN   [6]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
RA   Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT   "Determination of three isoforms of the receptor activator of nuclear
RT   factor-kappaB ligand and their differential expression in bone and
RT   thymus.";
RL   Endocrinology 142:1419-1426(2001).
RN   [7]
RP   PROTEIN SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
RX   MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
RA   Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
RA   Schloendorff J., Tempst P., Choi Y., Biobel C.P.;
RT   "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
RT   converting enzyme-like protease in shedding of TRANCE, a TNF family
RT   member involved in osteoclastogenesis and dendritic cell survival.";
RL   J. Biol. Chem. 274:13613-13618(1999).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
RX   MEDLINE=21464816; PubMed=11581298;
RA   Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.,
RT   "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
RT   of receptor-ligand specificity.";
RL   J. Clin. Invest. 108:971-979(2001).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
RX   MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M105252200;
RA   Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
RT   "Crystal structure of the extracellular domain of mouse RANK ligand at
RT   2.2-A resolution.";
RL   J. Biol. Chem. 277:6631-6636(2002).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC   TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC   Augments the ability of dendritic cells to stimulate naive T-cell
CC   proliferation. May be an important regulator of interactions
CC   between T cells and dendritic cells and may play a role in the
CC   regulation of the T cell-dependent immune response. May also play
CC   an important role in enhanced bone-resorption in humoral
CC   hypercalcemia of malignancy.
CC   -!- SUBUNIT: Homotrimer.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC   (isoforms 1 and 2); Cytoplasmic (isoform 3).
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=3;
CC   Name=1;
CC   IsoId=O35235-1; Sequence=Displayed;
CC   Name=2;
CC   IsoId=O35235-2; Sequence=VSP_006449;
CC   Name=3;
CC   IsoId=O35235-3; Sequence=VSP_006448;
CC   -!- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
CC   but not in nonlymphoid tissues and is abundantly expressed in T
CC   cells but not in B cells. A high level expression is also seen in
CC   the trabecular bone and lung.
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: The soluble form of isoform 1 derives from the membrane form

CC   by proteolytic processing. The cleavage may be catalyzed by
CC   ADAM17. A further shorter soluble form was observed.
CC   -!- DISEASE: Deficiency in Tnfsf11 results in failure to form lobulo-
CC   alveolar mammary structures during pregnancy, resulting in death
CC   of newborns. Trance-deficient mice show severe osteopetrosis, with
CC   no osteoclasts, marrow spaces, or tooth eruption, and exhibit
CC   profound growth retardation at several skeletal sites, including
CC   the limbs, skull, and vertebrae and have marked chondrodysplasia,
CC   with thick, irregular growth plates and a relative increase in
CC   hypertrophic chondrocytes.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.

DR   EMBL; AF013170; AAC71061.1; -; mRNA.
DR   EMBL; AF019048; AAB86812.1; -; mRNA.
DR   EMBL; AF053713; AAC40113.1; -; mRNA.
DR   EMBL; AB008426; BAA25425.1; -; mRNA.
DR   EMBL; AB022039; BAA36970.1; -; Genomic_DNA.
DR   EMBL; AB032771; BAA97257.1; -; mRNA.
DR   EMBL; AB032772; BAA97258.1; -; mRNA.
DR   EMBL; AB036798; BAA97259.1; -; mRNA.
DR   PDB; 1IQA; X-ray; A/B/C=157-316.
DR   PDB; 1JTZ; X-ray; X/Y/Z=156-316.
DR   Ensembl; ENSMUSG00000022015; Mus musculus.
DR   MGI; MGI:1100089; Tnfsf11.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0045453; P:bone resorption; IDA.
DR   GO; GO:0007515; P:lymph gland development; IDA.
DR   GO; GO:0009887; P:organogenesis; IMP.
DR   GO; GO:0001503; P:ossification; IMP.
DR   GO; GO:0045672; P:positive regulation of osteoclast different...; IDA.
DR   GO; GO:0051260; P:protein homooligomerization; IDA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD020012; TNF; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   3D-structure; Alternative splicing; Cytokine; Developmental protein;
KW   Differentiation; Direct protein sequencing; Glycoprotein; Receptor;
KW   Signal-anchor; Transmembrane.

FT   CHAIN   1   316   Tumor necrosis factor ligand superfamily
FT   member 11, membrane form.
FT   CHAIN   139   316   Tumor necrosis factor ligand superfamily
FT   member 11, soluble form.
FT   TOPO_DOM   1   48   Cytoplasmic (Potential).
FT   TRANSMEM   49   69   Signal-anchor for type II membrane
FT   protein (Potential).
FT   TOPO_DOM   70   316   Extracellular (Potential).
FT   SITE   138   139   Cleavage.
FT   CARBOHYD   197   197   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   262   262   N-linked (GlcNAc...) (Potential).
FT   VARSPLIC   1   117   Missing (in isoform 3).
FT   /FTId=VSP_006448.
FT   VARSPLIC   14   44   SSEEMSSGPGVPHEGPLHPAPSAPAPPPA -> TP (in
FT   isoform 2).
FT   /FTId=VSP_006449.
FT   CONFLICT   99   99   G -> D (in Ref. 2).
FT   CONFLICT   141   143   Missing (in Ref. 5).
FT   STRAND   164   169
FT   TURN   171   172
FT   STRAND   181   182
FT   STRAND   186   187
FT   TURN   191   191
FT   TURN   191   192
FT   STRAND   194   196
FT   STRAND   198   201

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OM protein - protein search, using sw model

Run on: December 21, 2005, 12:34:10 ; Search time 18.3689 seconds
                 (without alignments)
                 645.834 Million cell updates/sec

Title: US-09-211-297-32
Perfect score: 148
Sequence: 1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	148	100.0	27	2	AAW83196	Murine os
2	148	100.0	28	2	AAW83197	Murine os
3	148	100.0	155	6	ABR39854	RANK liga
4	148	100.0	155	7	ADC03334	Murine re
5	148	100.0	155	7	ADI53055	Human RAN
6	148	100.0	160	3	AAB08272	Amino aci
7	148	100.0	170	4	AAU08386	Mouse FLA
8	148	100.0	170	4	ADJ82132	Protein f
9	148	100.0	173	3	AAY84426	An osteop
10	148	100.0	173	3	AAY84422	A murine
11	148	100.0	173	3	AAY84425	DNA encod
12	148	100.0	173	3	AAY84421	Amino aci
13	148	100.0	182	3	AAY84424	An osteop
14	148	100.0	187	3	AAY84420	Amino aci
15	148	100.0	188	3	AAY84423	An osteop
16	148	100.0	193	7	ADJ82129	Protein f
17	148	100.0	199	5	ABG94285	Mouse RAN
18	148	100.0	199	5	ABG80597	Mouse rec
19	148	100.0	199	7	ADJ82119	Protein f
20	148	100.0	216	7	ADB16999	Murine RA
21	148	100.0	244	2	AAW83019	A murine
22	148	100.0	244	5	ABG94284	Mouse RAN
23	148	100.0	247	5	ABG80596	Mouse rec
24	148	100.0	247	7	ADJ82118	Protein f
25	148	100.0	249	6	ADA50081	Mouse wil
26	148	100.0	294	2	AAW69956	NF-kB rec
27	148	100.0	294	2	AAW68292	NF-kB rec
28	148	100.0	294	2	AAE08737	Murine re
29	148	100.0	294	4	AAE04425	Murine re
30	148	100.0	294	4	AAE01992	Murine RA
31	148	100.0	294	7	AAE26102	Mouse RAN
32	148	100.0	294	7	ADB16986	Murine re
33	148	100.0	294	7	ADC73000	Murine RA
34	148	100.0	294	7	ADC78266	Murine RA
35	148	100.0	294	7	ADG46721	Murine RA
36	148	100.0	294	9	ADW09027	Murine re
37	148	100.0	316	2	AAW83017	Osteoclas
38	148	100.0	316	2	AAW83194	Human ost
39	148	100.0	316	2	AAW59654	Amino aci
40	148	100.0	316	2	AAY17874	Murine TR
41	148	100.0	316	3	AAY91024	Mouse OBM
42	148	100.0	316	3	AAY84418	Amino aci
43	148	100.0	316	3	AAY84419	Amino aci
44	148	100.0	316	5	AAU78289	Mouse TRA
45	148	100.0	316	5	ADR29338	Mouse RAN

ALIGNMENTS

RESULT 1
AAW83196
ID   AAW83196 standard; peptide; 27 AA.
XX
AC   AAW83196;
XX
DT   11-FEB-1999 (first entry)
XX
DE   Murine osteoprotegerin binding protein BB' loop peptide.
XX
KW   Osteoprotegerin binding protein; OPG binding protein; arthritis;
KW   osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW   hypercalcaemia; osteoclast differentiation and activation receptor;
KW   Paget's disease.
XX
OS   Mus sp.
XX
PN   WO9846751-A1.
XX
PD   22-OCT-1998.
XX
PF   15-APR-1998;   98WO-US007584.
XX
PR   16-APR-1997;   97US-00842842.
PR   23-JUN-1997;   97US-00880855.
PR   30-MAR-1998;   98US-00052521.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ;
XX
PT   WPI; 1998-594578/50.
XX
DR   Example 11; Page 55; 47pp; English.
XX
PS   Example 11; Page 55; 47pp; English.
XX
CC   The present sequence represents peptide from murine osteoprotegerin (OPG)
CC   binding protein. Host cells transfected with vectors containing nucleic
CC   acid molecules encoding OPG binding protein are used to produce
CC   recombinant OPG binding protein. OPG binding protein is used in binding
CC   assays to determine osteoprotegerin (OG) in biological samples; to screen
CC   for specific binding agents (particularly agonists and antagonists,
CC   including intracellular proteins); to raise Ab (useful in immunoassays
CC   for detection of OPG binding protein) and to identify compounds that

CC modulate binding of OPG binding protein to osteoclast differentiation and
CC activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC binding protein can be used to detect OPG binding protein-encoding
CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models while complementary sequences are used for
CC antisense regulation of OPG binding protein expression. Modulators of OPG
CC binding protein, particularly soluble forms of OPG binding protein or Ab,
CC are used to treat or prevent bone diseases e.g. osteoporosis, bone loss
CC caused by arthritis or metastases, hypercalcaemia, Paget's disease,
CC periodontal disease, osteoporosis, loosening of prostheses, optionally in
CC combination with agents that promote bone growth
XX

SQ Sequence 27 AA;

Qy   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
       |||||||||||||||||||||||||||
Db   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

Query Match   100.0%; Score 148; DB 2; Length 27;
Best Local Similarity   100.0%; Pred. No. 7.8e-16;
Matches   27; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

SQ Sequence 27 AA;

RESULT 2
ID   AAW83197 standard; peptide; 28 AA.
XX
AC   AAW83197;
XX
DT   11-FEB-1999 (first entry)
XX
DE   Murine osteoprotegerin binding protein BB' loop-Cys peptide.
XX
KW   osteoprotegerin binding protein; OPG binding protein; arthritis;
KW   osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW   hypercalcaemia; osteoclast differentiation and activation receptor;
KW   Paget's disease.
XX
OS   Mus sp.
XX
PN   WO9846751-A1.
XX
PD   22-OCT-1998.
XX
PF   15-APR-1998;   98WO-US007584.
PR   16-APR-1997; 97US-00842842.
PR   23-JUN-1997; 97US-00880855.
PR   30-MAR-1998; 98US-00052521.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ;
XX
DR   WPI; 1998-594578/50.
XX
PT   Nucleic acid encoding osteoprotegerin binding protein - useful for, e.g.
PT   treating bone diseases by modulating osteoclast differentiation and for
PT   diagnosis.
XX
PS   Example 11; Page 55; 47pp; English.
XX
CC   The present sequence represents peptide from murine osteoprotegerin (OPG)
CC   binding protein. Host cells transfected with vectors containing nucleic
CC   acid molecules encoding OPG binding protein are used to produce
CC   recombinant OPG binding protein. OPG binding protein is used in binding
CC   assays to determine osteoprotegerin (OG) in biological samples; to screen
CC   for specific binding agents (particularly agonists and antagonists,
CC   including intracellular proteins); to raise Ab (useful in immunoassays
CC   for detection of OPG binding protein) and to identify compounds that
CC   modulate activation of OPG binding protein to osteoclast differentiation and
CC   activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC   binding protein can be used to detect OPG binding protein-encoding

---

CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models, while complementary sequences are used for
CC antisense regulation of OPG binding protein expression. Modulators of OPG
CC binding protein, particularly soluble forms of OPG binding protein or Ab,
CC are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss
CC caused by arthritis or metastases, hypercalcaemia, Paget's disease,
CC periodontal disease, osteoporosis, loosening of prostheses, optionally in
CC combination with agents that promote bone growth
XX

SQ Sequence 28 AA;

Qy   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
       |||||||||||||||||||||||||||
Db   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

Query Match   100.0%; Score 148; DB 2; Length 28;
Best Local Similarity   100.0%; Pred. No. 8.1e-16;
Matches   27; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

SQ Sequence 28 AA;

RESULT 3
ID   ABR39854 standard; protein; 155 AA.
XX
AC   ABR39854;
XX
DT   11-AUG-2003 (first entry)
XX
DE   RANK ligand (RANKL) protein fragment.
XX
KW   RANK; receptor activator of necrosis factor kB; RANK ligand; RANKL;
KW   mouse.
XX
OS   Mus sp.
XX
PN   WO200301407-A2.
XX
PD   20-FEB-2003.
XX
PF   09-AUG-2002; 2002WO-US025287.
XX
PR   09-AUG-2001; 2001US-0311163P.
PR   22-MAR-2002; 2002US-00105057.
XX
PA   (BARN-) BARNES-JEWISH HOSPITAL.
XX
PI   Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;
XX
DR   WPI; 2003-256526/25.
XX
PT   Composition for identifying a compound with Receptor Activator of
PT   Necrosis Factor kB, RANK modulating activity and for identifying RANK or
PT   osteoprotegerin modulating compound, has a protein complex in crystalline
PT   form.
XX
PS   Disclosure; Fig 3; 66pp; English.
XX
CC   The invention relates to a composition (I) comprising a protein complex
CC   in crystalline form, where the complex comprises an amino acid sequence
CC   of a Receptor Activator of Necrosis Factor kB (RANK) Ligand (RANKL)
CC   ectodomain. (I) is useful for identifying a compound with RANK modulating
CC   activity, and for identifying a RANK or OPG modulating compound. (I) is
CC   useful to intelligently design mutants that have altered biological
CC   properties and for identifying and/or designing compounds that bind RANK
CC   as an approach towards developing new therapeutic agents. (I) is also
CC   useful to computationally screen small molecule databases for chemical
CC   entities or compounds that can bind in whole, or in part, to RANK or
CC   RANKL. The present sequence represents a murine RANKL protein fragment
XX

SQ Sequence 155 AA;

Query Match   100.0%; Score 148; DB 6; Length 155;
Best Local Similarity   100.0%; Pred. No. 6.6e-15;

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:47:51 ; Search time 3.0541 Seconds
            (without alignments)
            850.612 Million cell updates/sec

Title: US-09-211-297-32
Perfect score: 148
Sequence: 1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Databases :   PIR_80:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	59	39.9	456	2	AC3323	manganese transpor
2	49	33.1	369	2	C97484	outer membrane pro
3	49	33.1	369	2	AC2702	outer membrane pro
4	49	33.1	417	2	A96610	probable pectinate
5	49	33.1	747	2	F87263	TPR domain protein
6	49	33.1	780	2	G72724	probable penicilli
7	49	33.1	827	1	A36895	endopeptidase La (
8	48.5	32.8	199	2	AD24886	hypothetical prote
9	48.5	32.8	570	2	E29525	methyl coenzyme M
10	48	32.4	245	2	B86889	zinc ABC transport
11	48	32.4	452	2	E84186	hypothetical prote
12	48	32.4	831	2	T00323	hypothetical prote
13	47.5	32.4	1888	2	T39009	hypothetical prote
14	47.5	32.1	197	2	B96568	hypothetical prote
15	47.5	32.1	230	2	A96565	hypothetical prote
16	47	31.8	398	2	I49443	gene 2B4 protein -
17	47	31.8	406	2	AG0548	probable ABC-trans
18	47	31.8	442	2	T50687	proline transport
19	47	31.8	442	2	S42864	protein kinase (EC
20	47	31.8	522	2	D96836	probable glycerol
21	47	31.8	576	2	A53982	capsid protein - E
22	47	31.8	693	2	A41617	dopamine transport
23	47	31.8	1520	2	T30820	carbamoyl-phosphat
24	46.5	31.4	172	2	E96518	protein T2E6.12 [i
25	46.5	31.4	637	2	A96568	hypothetical prote
26	46.5	31.4	637	2	S01509	NADH2 dehydrogenas
27	46	31.1	336	2	F84056	hypothetical prote
28	46	31.1	336	2	F95925	hypothetical prote
29	46	31.1	350	2	T32215	hypothetical prote
30	46	31.1	394	1	S77216	hypothetical prote
31	46	31.1	512	2	A54400	protein kinase (EC
32	46	31.1	605	1	Q0B83R	BVRF2 (EC-RF3) pro
33	46	31.1	686	2	T15795	hypothetical prote
34	45.5	30.7	263	2	AD0851	secretory protein
45.5	30.7	756	2	A13275	phosphoenolpyruvat
35	45	30.4	112	2	T38761	hypothetical prote
36	45	30.4	105	2	E83817	hypothetical prote
37	45	30.4	205	2	A75165	thymidylate kinase
38	45	30.4	205	2	C43670	integral membrane
39	45	30.4	278	2	A05062	probable mbpY prot
40	45	30.4	288	2	S58146	hypothetical prote
41	45	30.4	325	2	T40042	conserved hypothet
42	45	30.4	334	2	F90194	threonine synthase
43	45	30.4	345	2	AE2782	transcription regu
44	45	30.4	365	2	F97561	hypothetical prote
45	45	30.4	365	2		hypothetical prote

ALIGNMENTS

RESULT 1
AC3323
manganese transport protein mntH [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AC3323
R;Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
  .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AC3323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-456 <KUR>
A;Cross-references: UNIPROT:Q8YI76; UNIPARC:UPI00000057D23; GB:AE008917; PIDN:AAL51750.1;
A;Experimental source: strain 16M
A;Genetics:
A;Gene: BME10569
C;Superfamily: natural resistance-associated macrophage protein 1

Query Match   39.9%; Score 59; DB 2; Length 456;
Best Local Similarity 45.8%; Pred. No. 0.94;
Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy   4 SIPGGSHKVTLSSWYHDRGWAKIS 27
         |||| | ::|| | ||| :|
Db   6 SCPSGAREVTFEGWRRERGEASMS 29

RESULT 2
C97484
outer membrane protein a2 precursor [imported] - Agrobacterium tumefaciens (strain C58,
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97484
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
  .; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C97484
A;Status: preliminary
A;Molecule type: DNA
A;Residue: 1-369 <KUR>
A;Cross-references: UNIPROT:Q8UGL7; UNIPARC:UPI0000019FA; GB:AE007869; PIDN:AAK86828.1;
A;Genetics:
A;Gene: AGR_C_1878
A;Map position: circular chromosome

Query Match   33.1%; Score 49; DB 2; Length 369;

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Db  305 NAAGVPIGASAIITNDWSNRDAW 327
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Best Local Similarity 30.4%; Pred. No. 22;
Matches 7; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

RESULT 3
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C;Accession: AC2702
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Species: Agrobacterium tumefaciens
A;outer membrane protein Atu1020 [imported] - Agrobacterium tumefaciens (strain C58, Dupon
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC2702
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-369 <KUR>
A;Cross-references: UNIPROT:Q8UGL7; UNIPARC:UPI0000D19FA; GB:AE008688; PIDN:AAL42033.1;
C;Genetics:
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu1020
A;Map position: circular chromosome

Query Match 33.1%; Score 49; DB 2; Length 369;
Best Local Similarity 30.4%; Pred. No. 22;
Matches 7; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

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        |||:|:|::||:|::|||  |
Db  305 NAAGVPIGASAIITNDWSNRDAW 327
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RESULT 4
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C;Accession: A96610
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;probable pectinacetylesterase precursor T8L23.6 [imported] - Arabidopsis thaliana
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C;A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96610
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-417 <STO>
A;Cross-references: UNIPROT:Q9FVU3; UNIPARC:UPI00000483B1; GB:AE005173; NID:g11055858;
A;Gene: T8L23.6
C;Genetics:
A;Map position: 1

Query Match 34.6%; Score 49; DB 2; Length 417;
Best Local Similarity 30.4%; Pred. No. 25;
Matches 9; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

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Db  374 NSPAIKNKGIAVAVGDWYFERGGAKL 399
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RESULT 5
F87263
C;Accession: F87263
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Species: Caulobacter crescentus
A;TPR domain protein [imported] - Caulobacter crescentus
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F
B.J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Durkin, S.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: F87263
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87263
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-747 <STO>
A;Cross-references: UNIPROT:Q9ABV1; UNIPARC:UPI00000C6F34; GB:AE005673; NID:g13421226; P
A;Gene: CC0119
C;Genetics:

Query Match 33.1%; Score 49; DB 2; Length 747;
Best Local Similarity 43.5%; Pred. No. 46;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

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G72724
C;Accession: G72724
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Species: Aeropyrum pernix
A;probable penicillin acylase APE0336 - Aeropyrum pernix (strain K1)
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, Y.; Jin-no, K.; Takahe
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ka
DNA Res. 6, 83-101, 1999
A;Reference number: G72724
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyru
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G72724
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-780 <KAW>
A;Cross-references: UNIPROT:Q9YFA5; UNIPARC:UPI00000SDAD8; DDBJ:AP000059; NID:g5103911; P
C;Genetics:
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0336

Query Match 33.1%; Score 49; DB 2; Length 780;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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Qy    4 SIPSGSHKVTLSSWYHDRGW 23
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Db  734 SLPGGSSGVPLSSFYDNLYW 753
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RESULT 7
A36895
C;Accession: A36895
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004
C;Species: Myxococcus xanthus
A;endopeptidase La (EC 3.4.21.53) 2 - Myxococcus xanthus
N;Alternate names: ATP-dependent proteinase BsgA; ATP-dependent proteinase lonD; ATP-depe
N;Contains: adenosinetriphosphatase (EC 3.6.1.3)
R;Tojo, N.; Inouye, S.; Komano, T.
J. Bacteriol. 175, 4545-4549, 1993
A;Title: The lonD gene is homologous to the lon gene encoding an ATP-dependent protease a
A;Reference number: A36895; MUID:93322335; PMID:8331083

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:44:31 ; Search time 4.60328 seconds

484.925 Million cell updates/sec
(without alignments)

Title: US-09-211-297-32
Perfect score: 148
Sequence: 1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
Scoring table: BLOSUM62
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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	ID	Description
1	148	100.0	28	2	US-09-052-521C-34	Sequence 34, Appl
2	148	100.0	77	2	US-09-632-287A-10	Sequence 10, Appl
3	148	100.0	77	2	US-10-286-696-10	Sequence 10, Appl
4	148	100.0	173	2	US-09-396-937-10	Sequence 10, Appl
5	148	100.0	173	2	US-09-396-937-12	Sequence 12, Appl
6	148	100.0	173	2	US-09-396-937-18	Sequence 18, Appl
7	148	100.0	173	2	US-09-396-937-20	Sequence 20, Appl
8	148	100.0	182	2	US-09-396-937-16	Sequence 16, Appl
9	148	100.0	187	2	US-09-396-937-8	Sequence 8, Appli
10	148	100.0	188	2	US-09-396-937-14	Sequence 14, Appl
11	148	100.0	294	2	US-08-996-139-11	Sequence 11, Appl
12	148	100.0	294	2	US-09-995-659-11	Sequence 11, Appl
13	148	100.0	294	2	US-09-215-649A-11	Sequence 11, Appl
14	148	100.0	294	2	US-09-577-780-11	Sequence 11, Appl
15	148	100.0	294	2	US-09-577-800-11	Sequence 11, Appl
16	148	100.0	294	2	US-09-466-496-11	Sequence 11, Appl
17	148	100.0	294	2	US-09-871-856-11	Sequence 11, Appl
18	148	100.0	294	2	US-09-871-291-11	Sequence 11, Appl
19	148	100.0	294	2	US-09-877-650-11	Sequence 11, Appl
20	148	100.0	294	2	US-09-865-363-11	Sequence 11, Appl
21	148	100.0	294	2	US-09-688-459-11	Sequence 11, Appl
22	148	100.0	316	1	US-08-842-842-7	Sequence 7, Appli
23	148	100.0	316	2	US-08-989-362-2	Sequence 2, Appli
24	148	100.0	316	2	US-09-052-521C-2	Sequence 2, Appli
25	148	100.0	316	2	US-09-671-658A-2	Sequence 2, Appli
26	148	100.0	316	2	US-09-396-937-4	Sequence 4, Appli
27	148	100.0	316	2	US-09-396-937-6	Sequence 6, Appli
28	148	100.0	316	2	US-09-957-944-8	Sequence 8, Appli
29	136	91.9	77	2	US-09-632-287A-11	Sequence 11, Appl
30	136	91.9	77	2	US-10-286-696-11	Sequence 11, Appl
31	136	91.9	317	2	US-08-996-139-13	Sequence 13, Appl
32	136	91.9	317	2	US-09-995-659-13	Sequence 13, Appl
33	136	91.9	317	2	US-09-215-649A-13	Sequence 13, Appl
34	136	91.9	317	2	US-09-052-521C-4	Sequence 4, Appli
35	136	91.9	317	2	US-09-052-521C-33	Sequence 33, Appl
36	136	91.9	317	2	US-09-577-780-13	Sequence 13, Appl
37	136	91.9	317	2	US-09-577-800-13	Sequence 13, Appl
38	136	91.9	317	2	US-09-466-496-13	Sequence 13, Appl
39	136	91.9	317	2	US-09-871-856-13	Sequence 13, Appl
40	136	91.9	317	2	US-09-871-291-13	Sequence 13, Appl
41	136	91.9	317	2	US-09-877-650-13	Sequence 13, Appl
42	136	91.9	317	2	US-09-865-363-13	Sequence 13, Appl
43	136	91.9	317	2	US-09-688-459-13	Sequence 13, Appl
44	136	91.9	317	2	US-09-957-944-6	Sequence 6, Appli
45	135	91.2	27	2	US-09-052-521C-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-09-052-521C-34

; Sequence 34, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
US-09-052-521C-34

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Best Local Similarity   100.0%;
Matches   27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-632-287A-10

; Sequence 10, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 65214220e1 Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0

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;   SEQ ID NO 10
;   LENGTH: 77
;   TYPE: PRT
;   ORGANISM: Mouse
    US-09-632-287A-10

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US-10-286-696-10
;   Sequence 10, Application US/10286696
;   Patent No. 6852839
;   GENERAL INFORMATION:
;     APPLICANT: Hsu, Hailing
;     APPLICANT: Wooden, Scott K
;     APPLICANT: Boyle, William J
;     TITLE OF INVENTION: Fhm, A No. 6852839e1 Member of the TNF Ligand Supergene Family
;     FILE REFERENCE: 01017/35550A
;     CURRENT APPLICATION NUMBER: US/10/286,696
;     PRIOR APPLICATION NUMBER: US 60/147,294
;     PRIOR FILING DATE: 1999-08-04
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;     SOFTWARE: Patentin Ver. 2.0
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;   ORGANISM: Mouse
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Db         14 NAASIPSGSHKVTLSSWYHDRGWAKIS 40

Query Match             100.0%;  Score 148;  DB 2;  Length 77;
Best Local Similarity   100.0%;  Pred. No. 1.9e-14;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


RESULT 4
US-09-396-937-10
;   Sequence 10, Application US/09396937
;   Patent No. 6645500
;   GENERAL INFORMATION:
;     APPLICANT: M&E Biotech A/S
;     APPLICANT: HALKIER, Torben
;     APPLICANT: HAANING, Jesper
;     TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
;     FILE REFERENCE: 22021 PC 1
;     CURRENT APPLICATION NUMBER: US/09/396,937
;     CURRENT FILING DATE: 1999-09-15
;     NUMBER OF SEQ ID NOS: 35
;     SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 10
;   LENGTH: 173
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: DNA encoding
;     OTHER INFORMATION: murine OPGL, residues 158-316, fused to His tag
    US-09-396-937-10

Qy          1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
              ||||||||||||||||||||||||||||
Db         14 NAASIPSGSHKVTLSSWYHDRGWAKIS 40

Query Match             100.0%;  Score 148;  DB 2;  Length 173;
Best Local Similarity   100.0%;  Pred. No. 5e-14;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


RESULT 5
US-09-396-937-12
;   Sequence 12, Application US/09396937
;   Patent No. 6645500
;   GENERAL INFORMATION:
;     APPLICANT: M&E Biotech A/S
;     APPLICANT: HALKIER, Torben
;     APPLICANT: HAANING, Jesper
;     TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
;     FILE REFERENCE: 22021 PC 1
;     CURRENT APPLICATION NUMBER: US/09/396,937
;     CURRENT FILING DATE: 1999-09-15
;     NUMBER OF SEQ ID NOS: 35
;     SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 12
;   LENGTH: 173
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: Fusion of
;     OTHER INFORMATION: murine OPGL, residues 158-316 with C to S
;     OTHER INFORMATION: mutation, and His tag
    US-09-396-937-12

Qy          1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
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Db         27 NAASIPSGSHKVTLSSWYHDRGWAKIS 53

Query Match             100.0%;  Score 148;  DB 2;  Length 173;
Best Local Similarity   100.0%;  Pred. No. 5e-14;
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RESULT 6
US-09-396-937-18
;   Sequence 18, Application US/09396937
;   Patent No. 6645500
;   GENERAL INFORMATION:
;     APPLICANT: M&E Biotech A/S
;     APPLICANT: HALKIER, Torben
;     APPLICANT: HAANING, Jesper
;     TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
;     FILE REFERENCE: 22021 PC 1
;     CURRENT APPLICATION NUMBER: US/09/396,937
;     CURRENT FILING DATE: 1999-09-15
;     NUMBER OF SEQ ID NOS: 35
;     SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 18
;   LENGTH: 173
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: Fusion between
;     OTHER INFORMATION: murine OPGL, residues 158-316 with tetanus toxoid
;     OTHER INFORMATION: P2 epitope introduced, and His tag
    US-09-396-937-18

Qy          1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
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Db         27 NAASIPSGSHKVTLSSWYHDRGWAKIS 53

Query Match             100.0%;  Score 148;  DB 2;  Length 173;
Best Local Similarity   100.0%;  Pred. No. 5e-14;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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OM protein - protein search, using sw model

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                                GenCore version 5.1.6
                        Copyright (c) 1993 - 2005 Compugen Ltd.
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Perfect score: 148
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
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2	148	100.0	28	5	US-10-825-898-34	Sequence 34, Appl
3	148	100.0	77	4	US-10-286-696-10	Sequence 10, Appl
4	148	100.0	77	5	US-10-890-368-10	Sequence 10, Appl
5	148	100.0	77	5	US-10-889-948-10	Sequence 14, Appl
6	148	100.0	160	3	US-09-779-050A-14	Sequence 14, Appl
7	148	100.0	170	3	US-09-791-153A-76	Sequence 76, Appl
8	148	100.0	170	4	US-10-289-456-99	Sequence 99, Appl
9	148	100.0	173	4	US-10-664-801-10	Sequence 10, Appl
10	148	100.0	173	4	US-10-664-801-12	Sequence 12, Appl
11	148	100.0	173	4	US-10-664-801-18	Sequence 18, Appl
12	148	100.0	173	4	US-10-664-801-20	Sequence 20, Appl
13	148	100.0	182	4	US-10-664-801-16	Sequence 16, Appl
14	148	100.0	187	4	US-10-664-801-8	Sequence 8, Appl
15	148	100.0	188	4	US-10-664-801-14	Sequence 14, Appl
16	148	100.0	193	4	US-10-289-456-96	Sequence 96, Appl
17	148	100.0	199	4	US-10-050-902-224	Sequence 224, App
18	148	100.0	199	4	US-10-050-898-224	Sequence 224, Appl
19	148	100.0	199	4	US-10-289-456-86	Sequence 86, Appl
20	148	100.0	244	4	US-10-167-182-16	Sequence 16, Appl
21	148	100.0	244	4	US-10-460-623-16	Sequence 16, Appl
22	148	100.0	244	5	US-11-135-521-16	Sequence 16, Appl
23	148	100.0	244	5	US-10-854-300-16	Sequence 16, App
24	148	100.0	247	6	US-11-050-050-223	Sequence 223, App
25	148	100.0	247	4	US-10-050-898-223	Sequence 223, Appl
26	148	100.0	247	4	US-10-289-456-85	Sequence 85, Appli
27	148	100.0	249	4	US-10-338-785A-3	Sequence 3, Appli
28	148	100.0	249	4	US-10-611-363-3	Sequence 3, Appli
29	148	100.0	294	3	US-09-871-856-11	Sequence 11, Appl
30	148	100.0	294	3	US-09-865-363-11	Sequence 11, Appl
31	148	100.0	294	3	US-09-871-291-11	Sequence 11, Appl
32	148	100.0	294	3	US-09-877-650-11	Sequence 11, Appl
33	148	100.0	294	4	US-10-405-878-11	Sequence 11, Appl
34	148	100.0	294	5	US-10-802-133-11	Sequence 11, Appl
35	148	100.0	294	4	US-09-957-944-8	Sequence 8, Appl
36	148	100.0	316	3	US-09-957-944-7	Sequence 7, Appl
37	148	100.0	316	3	US-09-873-829-4	Sequence 4, Appl
38	148	100.0	316	3	US-09-933-915A-16	Sequence 16, Appli
39	148	100.0	316	4	US-10-017-910-4	Sequence 4, Appli
40	148	100.0	316	4	US-10-105-057-2	Sequence 2, Appli
41	148	100.0	316	4	US-10-272-411-19	Sequence 19, Appl
42	148	100.0	316	4	US-10-272-328A-19	Sequence 19, Appl
43	148	100.0	316	4	US-10-326-052-2	Sequence 2, Appli
44	148	100.0	316	4	US-10-167-182-1	Sequence 1, Appli
45	148	100.0	316	4	US-10-460-623-1	Sequence 1, Appli
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## ALIGNMENTS

RESULT 1
US-10-825-898-33

; Sequence 33, Application US/10825898
; Publication No. US2005000340A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS
; FILE REFERENCE: A-451K REV 09-10-03 54SEQ
; CURRENT APPLICATION NUMBER: US/10/825,898
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US/10/825,898
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US 09/052,521
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: US 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: US 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 33
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-825-898-33

Query Match        100.0%;  Score 148;  DB 5;  Length 27;
Best Local Similarity   100.0%;
Matches   27;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db          1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

RESULT 2
US-10-825-898-34

; Sequence 34, Application US/10825898
; Publication No. US2005000340A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS
; FILE REFERENCE: A-451K REV 09-10-03 54SEQ
; CURRENT APPLICATION NUMBER: US/10/825,898
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US/10/825,898
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US 09/052,521

; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: US 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: US 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 34
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-825-898-34

Qy    Query Match             100.0%;  Score 148;  DB 5;  Length 28;
Db    Best Local Similarity   100.0%;  Pred. No. 7.1e-13;
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Db    1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

RESULT 3
US-10-286-696-10
; Sequence 10, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. US20030129706A1e1 Member of the TNF Ligand Supergene F
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Mouse
US-10-286-696-10

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Db    Best Local Similarity   100.0%;  Pred. No. 2e-12;
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Db   14 NAASIPSGSHKVTLSSWYHDRGWAKIS 40

RESULT 4
US-10-890-368-10
; Sequence 10, Application US/10890368
; Publication No. US20040248224A1
; GENERAL INFORMATION:
; APPLICANT: Hsu et al.
; TITLE OF INVENTION: FHM, A NOVEL MEMBER OF THE TNF LIGAND SUPERGENE FAMILY: MATERIALS
; TITLE OF INVENTION: METHODS FOR INTERACTION MODULATORS
; FILE REFERENCE: 01017/35550D
; CURRENT APPLICATION NUMBER: US/10/890,368
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US 10/286,696
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 09/632,287
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Mouse
US-10-890-368-10

Qy    Query Match             100.0%;  Score 148;  DB 5;  Length 77;
Db    Best Local Similarity   100.0%;  Pred. No. 2e-12;
      Matches   27;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Db   14 NAASIPSGSHKVTLSSWYHDRGWAKIS 40

RESULT 5
US-10-889-948-10
; Sequence 10, Application US/10889948
; Publication No. US20040265913A1
; GENERAL INFORMATION:
; APPLICANT: Hsu et al.
; TITLE OF INVENTION: FHM, A NOVEL MEMBER OF THE TNF LIGAND SUPERGENE FAMILY: MATERIALS AND METHODS
; FILE REFERENCE: 01017/35550C
; CURRENT APPLICATION NUMBER: US/10/889,948
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US 10/286,696
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 09/632,287
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Mouse
US-10-889-948-10

Qy    Query Match             100.0%;  Score 148;  DB 5;  Length 77;
Db    Best Local Similarity   100.0%;  Pred. No. 2e-12;
      Matches   27;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Db   14 NAASIPSGSHKVTLSSWYHDRGWAKIS 40

RESULT 6
US-09-779-050A-14
; Sequence 14, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 14
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-050A-14

Qy    Query Match             100.0%;  Score 148;  DB 3;  Length 160;
Db    Best Local Similarity   100.0%;  Pred. No. 4.2e-12;

OM protein - protein search, using sw model

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Run on: December 21, 2005, 13:03:52 ; Search time 0.840984 Seconds
228.978 Million cell updates/sec

Title: US-09-211-297-32
Perfect score: 148
Sequence: 1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match Length | DB | ID | Description |
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| 1 | 132 | 89.2 | 109 | 7 | US-11-065-669-8 | Sequence 8, Appli |
| 2 | 53.5 | 36.1 | 1649 | 6 | US-10-995-561-974 | Sequence 974, App |
| 3 | 53.5 | 36.1 | 1694 | 6 | US-11-135-855-36 | Sequence 36, Appl |
| 4 | 53.5 | 36.1 | 1709 | 6 | US-10-995-561-973 | Sequence 973, App |
| 5 | 53.5 | 36.1 | 1709 | 7 | US-11-135-855-35 | Sequence 35, Appl |
| 6 | 46 | 31.1 | 532 | 7 | US-10-152-747-2 | Sequence 2, Appli |
| 7 | 45 | 30.4 | 53 | 6 | US-10-467-657-4496 | Sequence 4496, Ap |
| 8 | 44 | 29.7 | 401 | 6 | US-10-510-386-68 | Sequence 68, Appl |
| 9 | 43.5 | 29.4 | 367 | 6 | US-10-821-234-1569 | Sequence 1569, App |
| 10 | 43.5 | 29.4 | 401 | 7 | US-11-097-749-3 | Sequence 3, Appli |
| 11 | 43.5 | 29.4 | 863 | 7 | US-10-793-626-2910 | Sequence 2910, Ap |
| 12 | 43 | 29.1 | 245 | 6 | US-11-097-749-2 | Sequence 2, Appli |
| 13 | 43 | 29.1 | 588 | 6 | US-10-793-626-3328 | Sequence 3328, Ap |
| 14 | 42.5 | 28.7 | 447 | 6 | US-11-112-882-4 | Sequence 4, Appli |
| 15 | 41 | 27.7 | 272 | 6 | US-10-467-657-2730 | Sequence 2730, Ap |
| 16 | 41 | 27.7 | 288 | 6 | US-10-131-826A-316 | Sequence 316, App |
| 17 | 41 | 27.7 | 987 | 6 | US-10-770-726-61 | Sequence 61, Appl |
| 18 | 40.5 | 27.4 | 250 | 6 | US-10-454-437-388 | Sequence 388, App |
| 19 | 40.5 | 27.4 | 378 | 7 | US-11-080-091-3 | Sequence 3, Appli |
| 20 | 40.5 | 27.4 | 378 | 7 | US-11-080-091-11 | Sequence 11, Appl |
| 21 | 40.5 | 27.4 | 378 | 7 | US-11-087-177-39 | Sequence 39, Appl |
| 22 | 40.5 | 27.4 | 378 | 7 | US-11-087-177-41 | Sequence 41, Appl |
| 23 | 40.5 | 27.4 | 488 | 6 | US-10-821-234-1000 | Sequence 1000, Ap |
| 24 | 40 | 27.0 | 296 | 6 | US-11-074-176-166 | Sequence 166, App |
| 25 | 40 | 27.0 | 362 | 6 | US-10-821-234-1148 | Sequence 1148, Ap |
| 26 | 40 | 27.0 | 651 | 6 | US-10-821-234-1480 | Sequence 1480, Ap |
| 27 | 40 | 27.0 | 2261 | 6 | US-10-995-561-600 | Sequence 600, App |
| 28 | 40 | 27.0 | 2516 | 6 | US-10-647-956A-2 | Sequence 2, Appli |
| 29 | 39.5 | 26.7 | 343 | 7 | US-11-080-291-86 | Sequence 86, Appli |
| 30 | 39.5 | 26.7 | 393 | 6 | US-10-821-233-1043 | Sequence 1043, Ap |
| 31 | 39 | 26.4 | 199 | 6 | US-10-467-657-8058 | Sequence 8058, Ap |
| 32 | 39 | 26.4 | 261 | 6 | US-10-617-034A-12 | Sequence 12, Appli |
| 33 | 39 | 26.4 | 282 | 6 | US-10-467-657-810 | Sequence 810, Appl |
| 34 | 39 | 26.4 | 309 | 7 | US-11-109-156-24 | Sequence 24, Appli |
| 35 | 39 | 26.4 | 309 | 7 | US-11-109-156-39 | Sequence 39, Appli |
| 36 | 39 | 26.4 | 311 | 6 | US-10-821-234-1638 | Sequence 1638, Ap |
| 37 | 39 | 26.4 | 322 | 6 | US-10-467-657-1354 | Sequence 1354, Ap |
| 38 | 39 | 26.4 | 998 | 6 | US-10-878-556A-59 | Sequence 59, Appl |
| 39 | 39 | 26.4 | 1467 | 6 | US-11-091-334-9 | Sequence 9, Appli |
| 40 | 39 | 26.4 | 1467 | 6 | US-10-873-528-38 | Sequence 38, Appli |
| 41 | 38.5 | 26.0 | 366 | 7 | US-10-507-956-1 | Sequence 1, Appli |
| 42 | 38.5 | 26.0 | 484 | 6 | US-10-878-556A-67 | Sequence 67, Appl |
| 43 | 38.5 | 26.0 | 617 | 6 | US-10-467-657-6006 | Sequence 6006, Ap |
| 44 | 38.5 | 26.0 | 659 | 6 | US-10-467-657-6006 | Sequence 6006, Ap |
| 45 | 38 | 25.7 | 179 | 6 | US-10-467-657-122 | Sequence 122, App |

ALIGNMENTS

RESULT 1
US-11-065-669-8
Sequence 8, Application US/11065669
Publication No. US2005024441A1
GENERAL INFORMATION:
APPLICANT: MacKay, Fabienne
APPLICANT: Kalled, Susan
TITLE OF INVENTION: BAFF, INHIBITORS THEREOF AND THEIR USE IN THE
TITLE OF INVENTION: MODULATION OF B-CELL RESPONSE
FILE REFERENCE: 08201.0024-04000
CURRENT APPLICATION NUMBER: US/11/065,669
CURRENT FILING DATE: 2005-02-24
PRIOR APPLICATION NUMBER: 10/045,574
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 09/911,777
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/143,228
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: PCT/US00/01788
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/117,169
PRIOR FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-11-065-669-8

Query Match 89.2%;   Score 132; DB 7; Length 109;
Best Local Similarity 85.2%;
Matches 23; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db 11 NATDIPSGSHKVSLSSWYHDRGWGKIS 37
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Pred. No. 3.2e-12;

RESULT 2
US-10-995-561-974
Sequence 974, Application US/10995561
Publication No. US2005027205A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF

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; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 974
; LENGTH: 1649
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-974

Query Match     36.1%;
Best Local Similarity   31.2%;   Score 53.5; DB 6; Length 1649;
Matches 10;  Conservative  5; Mismatches  6; Indels 11; Gaps  1;

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RESULT 3
US-11-135-855-36

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; Sequence 36, Application US/11135855
; Publication No. US20050255557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM p.l.c.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-36

Query Match     36.1%;
Best Local Similarity   31.2%;   Score 53.5; DB 7; Length 1694;
Matches 10;  Conservative  5; Mismatches  6; Indels 11; Gaps  1;

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US-10-995-561-973

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; Sequence 973, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 973
; LENGTH: 1709
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-995-561-973

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Best Local Similarity   31.2%;   Score 53.5; DB 6; Length 1709;
Matches 10;  Conservative  5; Mismatches  6; Indels 11; Gaps  1;

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RESULT 5
US-11-135-855-35

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; Sequence 35, Application US/11135855
; Publication No. US20050255557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM p.l.c.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 1709
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-35

Query Match     36.1%;
Best Local Similarity   31.2%;   Score 53.5; DB 7; Length 1709;
Matches 10;  Conservative  5; Mismatches  6; Indels 11; Gaps  1;

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          |::|__|         :|_||:||||:_|
Db   1263 AAVPEGAPITVTCADPAAHAPTLYTWHNGRW 1294
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RESULT 6
US-11-152-747-2

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; Sequence 2, Application US/11152747
; Publication No. US20050251881A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours, Inc.
; APPLICANT: Cheng, Qiong
; APPLICANT: Tao, Luan
; TITLE OF INVENTION: CAROTENOID KETOLASE GENE
; FILE REFERENCE: CL-1849 US NA
; CURRENT APPLICATION NUMBER: US/11/152,747
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rhodococcus erythropolis AN12
US-11-152-747-2

Query Match     31.1%;
Best Local Similarity   39.3%;   Score 46; DB 7; Length 532;
Matches 11;  Conservative  4; Mismatches  7; Indels  6; Gaps  2;
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